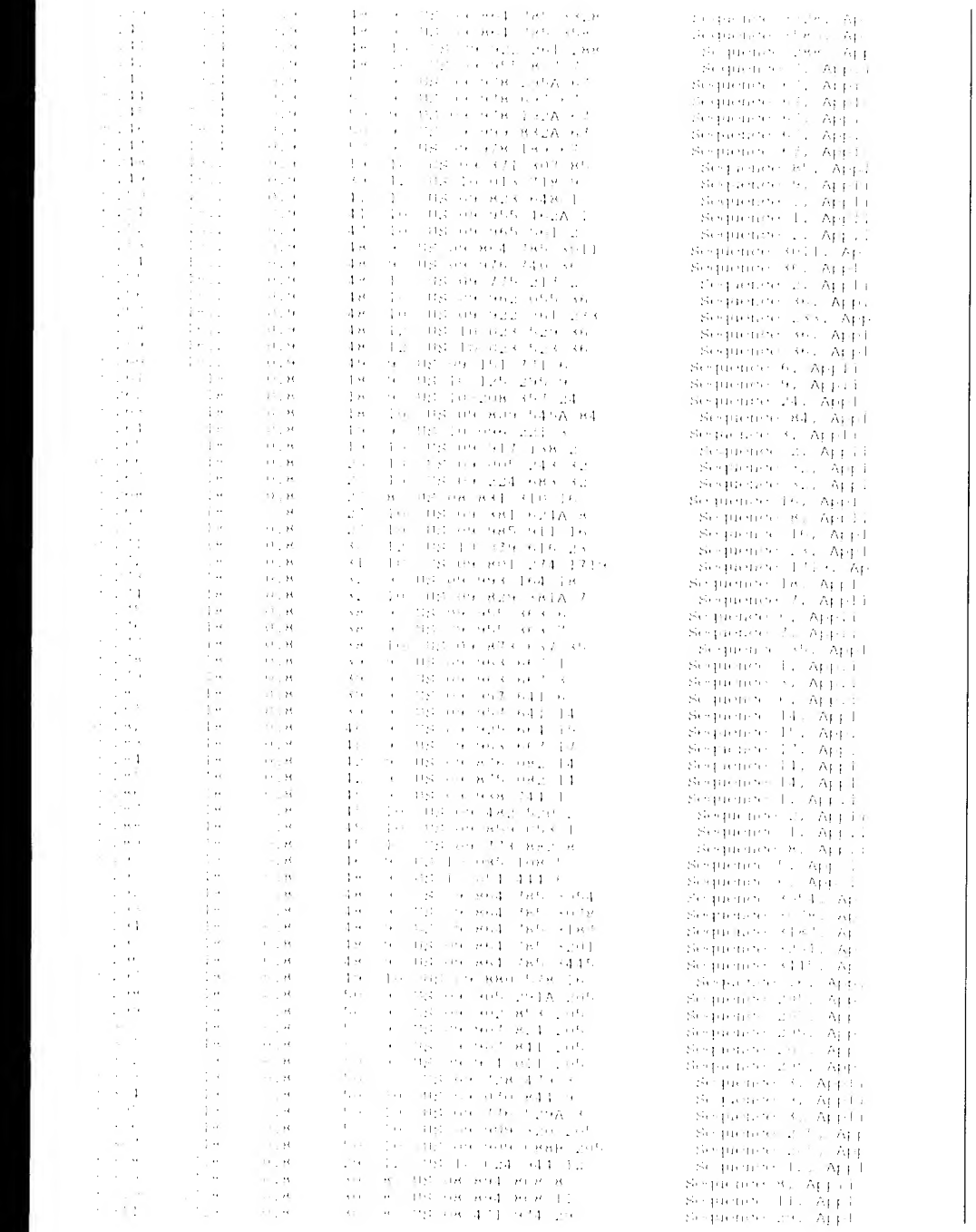

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495	17.2	0.8	41	10	US-09-858-369-11	Sequence 11, Appl
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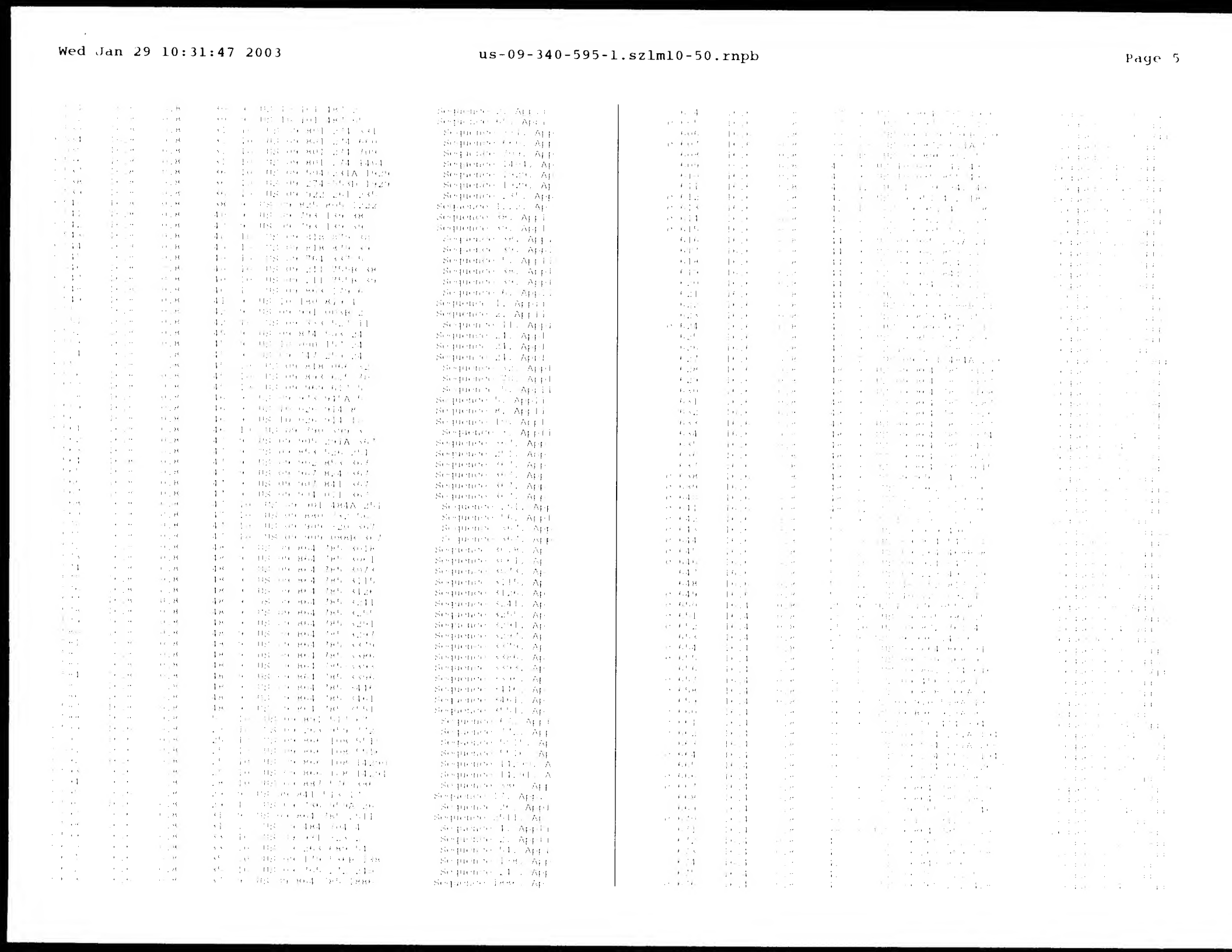

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	785	16.2	0.8	48	9	US-09-864-785-4274 Sequence 4274, Ap
	786	16.2	0.8	48	9	US-09-864-785-4284 Sequence 4284, Ap
	787	16.2	0.8	48	9	US-09-864-785-4314 Sequence 4314, Ap
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	789	16.2	0.8	48	9	US-09-864-785-4342 Sequence 4342, Ap
	790	16.2	0.8	48	9	US-09-864-785-4343 Sequence 4343, Ap
	791	16.2	0.8	48	9	US-09-864-785-4377 Sequence 4377, Ap
	792	16.2	0.8	48	9	US-09-864-785-4404 Sequence 4404, Ap
	793	16.2	0.8	48	9	US-09-864-785-4422 Sequence 4422, Ap
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	795	16.2	0.8	48	9	US-09-864-785-4541 Sequence 4541, Ap
	796	16.2	0.8	48	9	US-09-864-785-4549 Sequence 4549, Ap
	797	16.2	0.8	48	9	US-09-864-785-4565 Sequence 4565, Ap
	798	16.2	0.8	48	9	US-09-864-785-4574 Sequence 4574, Ap
	799	16.2	0.8	48	9	US-09-[illegible] Sequence 48, Appl
	800	16.2	0.8	48	10	US-09-[illegible] Sequence 48, Appl
	801	16.2	0.8	48	10	US-09-961-483A-2 Sequence 2, Appl
	802	16.2	0.8	48	10	US-09-[illegible] Sequence 48, Appl
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	806	16.2	0.8	50	9	US-09-943-[illegible] Sequence 122, Appl
	807	16.2	0.8	50	9	US-09-[illegible] Sequence 150, Appl
	808	16.2	0.8	50	9	US-09-[illegible] Sequence 155, Appl
	809	16.2	0.8	50	9	US-09-[illegible] Sequence 50, Appl
	810	16.2	0.8	50	9	US-09-[illegible] Sequence 50, Appl
	811	16.2	0.8	50	9	US-09-[illegible] Sequence 50, Appl
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	815	16.2	0.8	50	9	US-09-[illegible] Sequence 50, Appl
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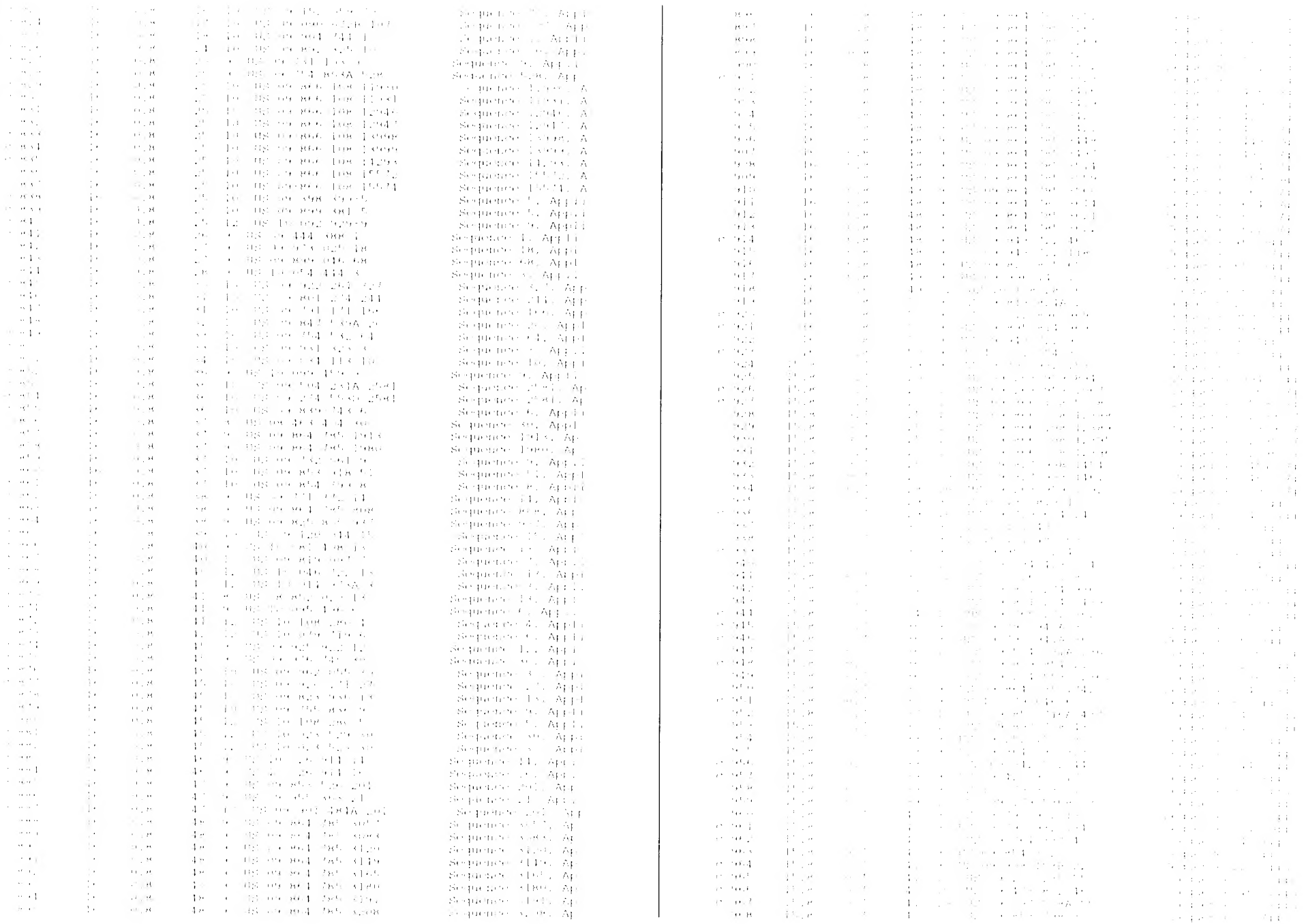

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971	15.8	0.7	42	10	US-09-759-272B-2	Sequence 2, Appli
972	15.8	0.7	42	10	US-09-480-226-16	Sequence 16, Appl
973	15.8	0.7	42	10	US-09-757-207-3	Sequence 3, Appli
974	15.8	0.7	43	9	US-09-794-699-11	Sequence 11, Appl
975	15.8	0.7	45	9	US-09-979-295A-135	Sequence 135, Ap
976	15.8	0.7	45	9	US-09-853-526-111	Sequence 111, App
977	15.8	0.7	45	9	US-09-979-762A-145	Sequence 145, App
978	15.8	0.7	45	9	US-09-979-762A-135	Sequence 135, Ap
979	15.8	0.7	45	9	US-09-999-842A-145	Sequence 145, Ap
980	15.8	0.7	45	9	US-09-978-189-135	Sequence 135, Ap
981	15.8	0.7	45	10	US-09-827-289-14	Sequence 14, Appl
982	15.8	0.7	45	10	US-09-901-484A-111	Sequence 111, App
983	15.8	0.7	47	9	US-09-853-526-197	Sequence 197, App
984	15.8	0.7	47	9	US-09-853-526-209	Sequence 209, App
985	15.8	0.7	47	9	US-09-853-526-303	Sequence 303, App
986	15.8	0.7	47	9	US-10-004-201-21	Sequence 21, Appl
987	15.8	0.7	47	9	US-09-496-041-4	Sequence 4, Appli
988	15.8	0.7	47	9	US-09-791-512-154	Sequence 154, App
989	15.8	0.7	47	10	US-09-740-092-4	Sequence 4, Appli
990	15.8	0.7	47	10	US-09-785-632A-7	Sequence 7, Appli
991	15.8	0.7	47	10	US-09-901-484A-197	Sequence 197, App
992	15.8	0.7	47	10	US-09-901-484A-209	Sequence 209, App
993	15.8	0.7	47	10	US-09-901-484A-303	Sequence 303, App
994	15.8	0.7	48	9	US-09-785-632A-[illegible]	Sequence [illegible], Ap
995	15.8	0.7	48	9	US-09-864-785-6006	Sequence 6006, Ap
996	15.8	0.7	48	9	US-09-864-785-[illegible]	Sequence [illegible], Ap
997	15.8	0.7	48	9	US-09-864-785-4065	Sequence 4065, Ap
998	15.8	0.7	48	9	US-09-864-785-4141	Sequence 4141, Ap
999	15.8	0.7	48	9	US-09-864-785-4145	Sequence 4145, Ap
1000	15.8	0.7	48	9	US-09-864-785-4151	Sequence 4151, Ap

ALIGNMENTS

RESULT 1
US-09-827-289-18/
; Sequence 18, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 45929-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194,913
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PI primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-18

Query Match 1.7%; Score 85.2; DB 10; Length 45;
Best Local Similarity 92.5%; Pred. No. 5.2;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
US-09-827-289-14/
; Sequence 14, Application US/09827289

; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 45929-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194,913
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PI primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-14

Query Match 1.7%; Score 85.2; DB 10; Length 45;
Best Local Similarity 92.5%; Pred. No. 5.2;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 3
US-09-827-289-21/
; Sequence 21, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 45929-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194,913
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PI primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-21

Query Match 1.7%; Score 85.2; DB 10; Length 45;
Best Local Similarity 92.5%; Pred. No. 5.2;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2004 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2143
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Db 45 TTATAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 4
US-09-827-289-14/
; Sequence 14, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 45929-55
; CURRENT APPLICATION NUMBER: US/09/827,289

; FEATURE:
; OTHER INFORMATION: sequence designed to act as a linker
US-09-340-595-10

Query Match 1.6%; Score 33.8; DB 9; Length 42;
Best Local Similarity 94.1%; Pred. No. 55;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35
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Db 9 AGAAAGTGATAAAAAAAAAAAAAAAAAAAAAAAA 43

RESULT 9
US-09-340-595-1012/c
; Sequence 1012, Application US/09340595
; Patent No. US20010055596A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xi, Jiaochun
; APPLICANT: Kim, Gordon E.
; TITLE OF INVENTION: METHODS AND MEDICAMENTS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/340,595
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1012
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-340-595-1012

Query Match 1.5%; Score 32.4; DB 10; Length 50;
Best Local Similarity 78.0%; Pred. No. 1.4e-02;
Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AAAATAAATAATTAGAAA 19
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Db 50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 10
US-09-340-595-2
; Sequence 2, Application US/09340595
; Patent No. US20020004771A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN0165
; CURRENT APPLICATION NUMBER: US/09/820,253
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-820-253-2

Query Match 1.5%; Score 31; DB 10; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32
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Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 11
US-09-828-034-3
; Sequence 3, Application US/09828034
; Patent No. US20020164714A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN 165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-3

Query Match 1.5%; Score 31; DB 10; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32
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Db 2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 12
US-09-827-289-13/c
; Sequence 13, Application US/09827289
; Patent No. US20020147328A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Adeno-Associated Virus (AAV) Vector
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 10020.55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,852
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-13

Query Match 1.4%; Score 30; DB 10; Length 45;
Best Local Similarity 96.9%; Pred. No. 3.2e-02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32
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RESULT 13
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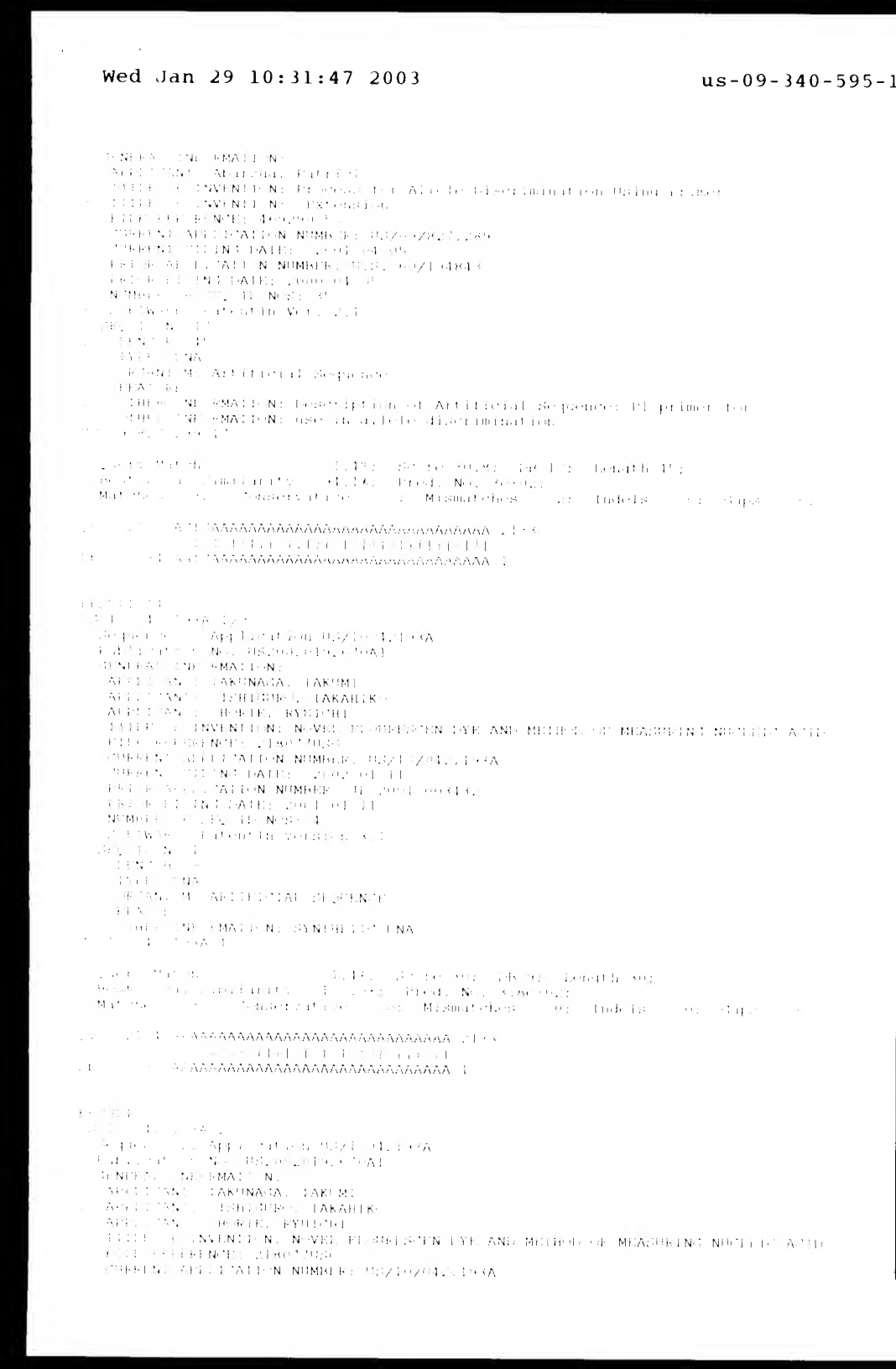
; Sequence 17, Application US/09827289
; Patent No. US20020147328A1



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  Matches   [illegible];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]


RESULT 19
US-09-836-077-19/c
; Sequence 19, Application US/09836077
; Patent No. US20020037851A1
;  GENERAL INFORMATION:
;        APPLICANT: FLECKENSTEIN, Bernhard
;                   ENSSER, Armin
;        TITLE OF INVENTION: HUMAN [illegible] AND
;                   CORRESPONDING [illegible] IN OTHER [illegible]
;        NUMBER OF SEQUENCES: 44
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Frommer Lawrence & Haug LLP
;             STREET: 745 Fifth Avenue
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10151
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/836,077
;             FILING DATE: 16 Apr 2001
;             CLASSIFICATION: Unknown
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lawrence, William F.
;             REGISTRATION NUMBER: 28,029
;             REFERENCE/DOCKET NUMBER: 514420-3647
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 212 588 0800
;             TELEFAX: 212 588 0500
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 50 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-836-077-19

  Query Match              1.4%;  Score 30;  DB 10;  Length 50;
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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


RESULT 19
US-09-896-856-5/c
; Sequence 5, Application US/09896856
; Patent No. US20020137139A1
;  GENERAL INFORMATION:
;        APPLICANT: Baker, Kevin
;                   Chien, Kenneth
;                   King, Kathleen
;                   Pennica, Diane
;                   Wood, William
;        TITLE OF INVENTION: [illegible]
;        NUMBER OF SEQUENCES: [illegible]
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: [illegible]
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: [illegible] floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible]
;             CLASSIFICATION: [illegible]
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] 1996
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible]-JUN 1996
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: 2?-APR 1994
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] APR 1994
;             APPLICATION NUMBER: 08/11[illegible]
;             FILING DATE: 17-MAY 199?
;        ATTORNEY/AGENT INFORMATION:
;             NAME: [illegible]
;             REGISTRATION NUMBER: [illegible]
;             REFERENCE/DOCKET NUMBER: [illegible]
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: [illegible]
;             TELEFAX: [illegible]
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: [illegible] base pairs
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-896-856-5

  Query Match              [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity    [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy       2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
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Db         50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


RESULT 20
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; Sequence 20, Application US/[illegible]
; Patent No. US20[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Abarzua, Patricio
;  TITLE OF INVENTION: Process for Allele Discrimination [illegible]
;  TITLE OF INVENTION: Extension
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 4?
;   TYPE: DNA
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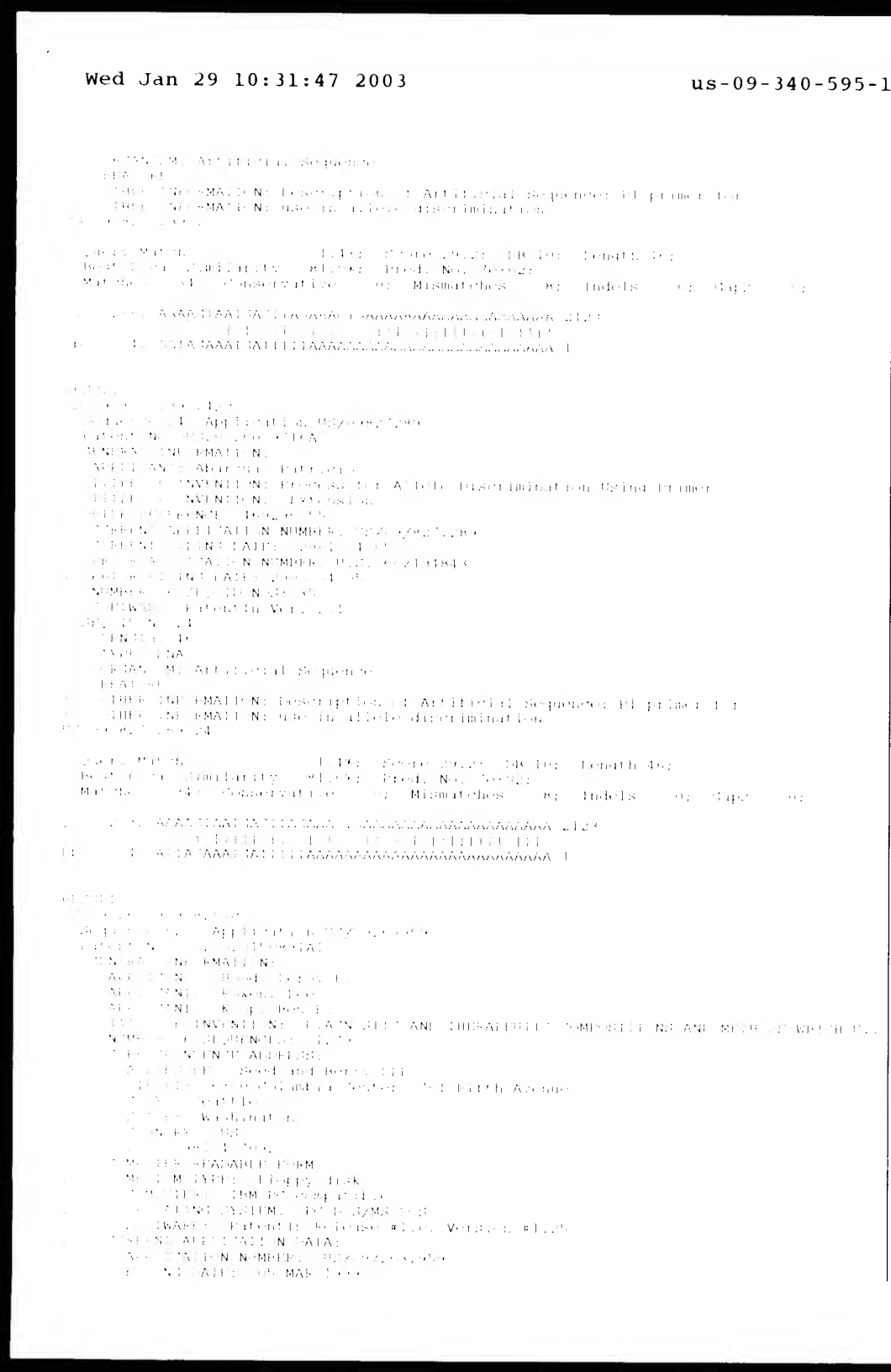

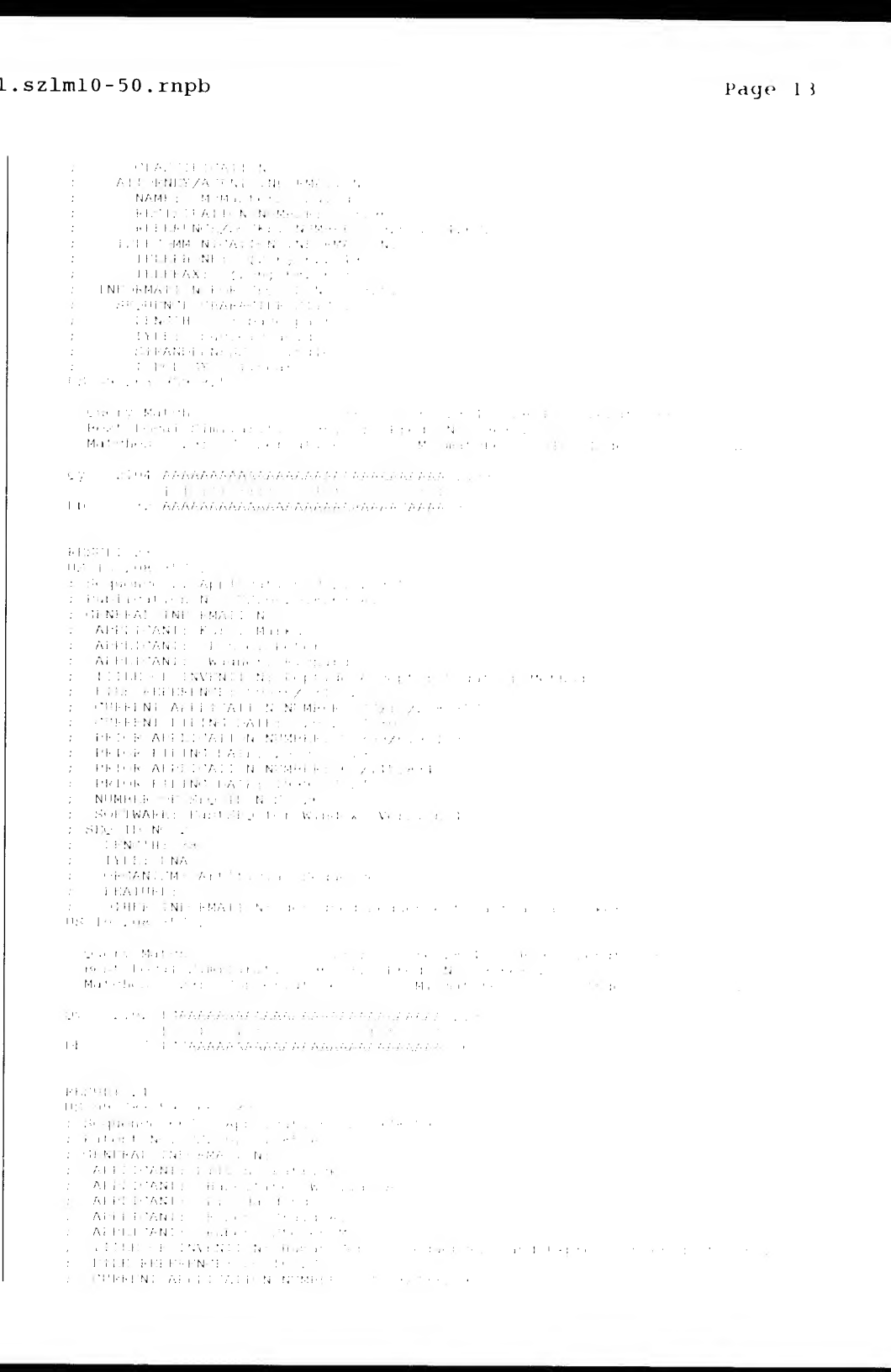

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;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 08/420,856
;  PRIOR FILING DATE: 1995-04-12
;  PRIOR APPLICATION NUMBER: 08/337,012
;  PRIOR FILING DATE: 1994-11-21
;  NUMBER OF SEQ ID NOS: 12485
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6670
;    LENGTH: 50
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (5)
;    OTHER INFORMATION: n equals a,t,g, or c
US-09-340-595-6670

  Query Match             1.4%;  Score 28.4;  DB 10;  Length 50;
  Best Local Similarity   96.7%;  Pred. No. 1.2e-05;
  Matches   29;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db      4 TTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11


RESULT 25
US-09-928-034-1
; Sequence 1, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
;  APPLICANT: Zhong, Weidong
;  APPLICANT:  Hong, Zhi
;  APPLICANT:  Ferrari, Eric
;  TITLE OF INVENTION: HCV REPLICASE COMPLEXES
;  FILE REFERENCE: IN01165
;  CURRENT APPLICATION NUMBER: US/09/928,034
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: U.S. 60/195,852
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
;    LENGTH: 40
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:Synthetic RNA
US-09-928-034-1

  Query Match             1.4%;  Score 28;  DB 10;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 29
          ||||||||||||||||||||||||||||
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 28


RESULT 26
US-10-208-457-5
; Sequence 5, Application US/10208457
; Publication No. US20020187967A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lobao, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 5036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,457
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/618,177
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: US/09/337,012
;  PRIOR FILING DATE: 1999-06-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;    LENGTH: 41
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-208-457-5

  Query Match             1.4%;  Score 28;  DB 10;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31
          ||||||||||||||||||||||||||||||
Db      4 TTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33


RESULT 27
US-10-208-457-4
; Sequence 4, Application US/10208457
; Publication No. US20020187967A1
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT:  Lobao, Peter
;  APPLICANT:  Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 5036/031002
;  CURRENT APPLICATION NUMBER: US/10/208,457
;  CURRENT FILING DATE:  2002-07-30
;  PRIOR APPLICATION NUMBER: US/09/618,177
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: US/09/337,012
;  PRIOR FILING DATE: 1999-06-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;    LENGTH: 40
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:Primer
US-10-208-457-4

  Query Match             1.4%;  Score 28;  DB 10;  Length 40;
  Best Local Similarity   96.6%;  Pred. No. 1.2e-05;
  Matches   28;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31
          ||||||||||||||||||||||||||||||
Db      3 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32


RESULT 28
US-09-827-252-7
; Sequence 7, Application US/09827252
; Patent No. US20020164797A1
; GENERAL INFORMATION:
;  APPLICANT: Akerstrom, Birgitta
;  TITLE OF INVENTION: Alpha-2-Macroglobulin-Like Protein 1
;  FILE REFERENCE: P01,0001
;  CURRENT APPLICATION NUMBER: US/09/827,252
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: US 60/195,193
;  PRIOR FILING DATE:  2000-04-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;    LENGTH: 45
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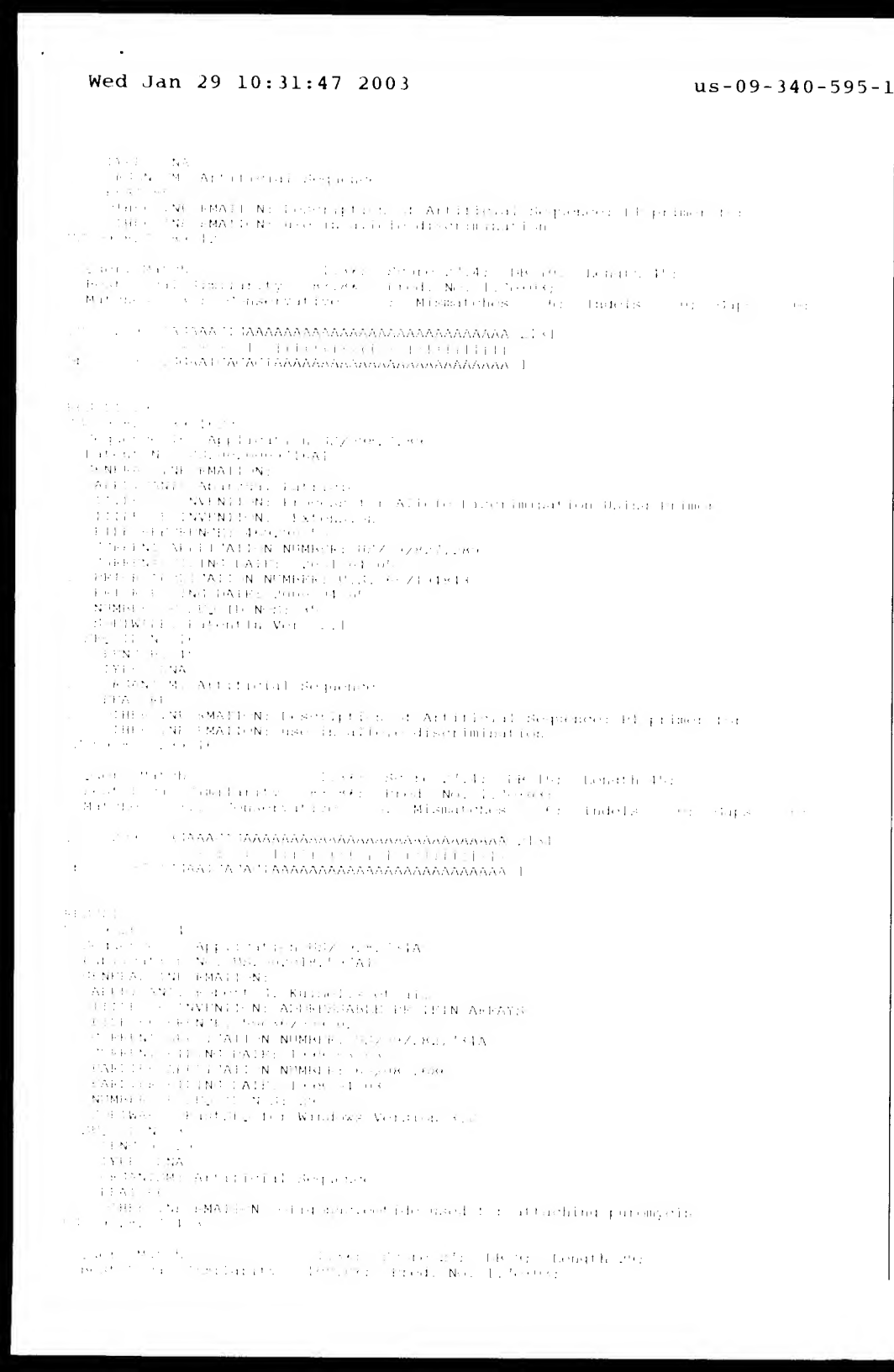

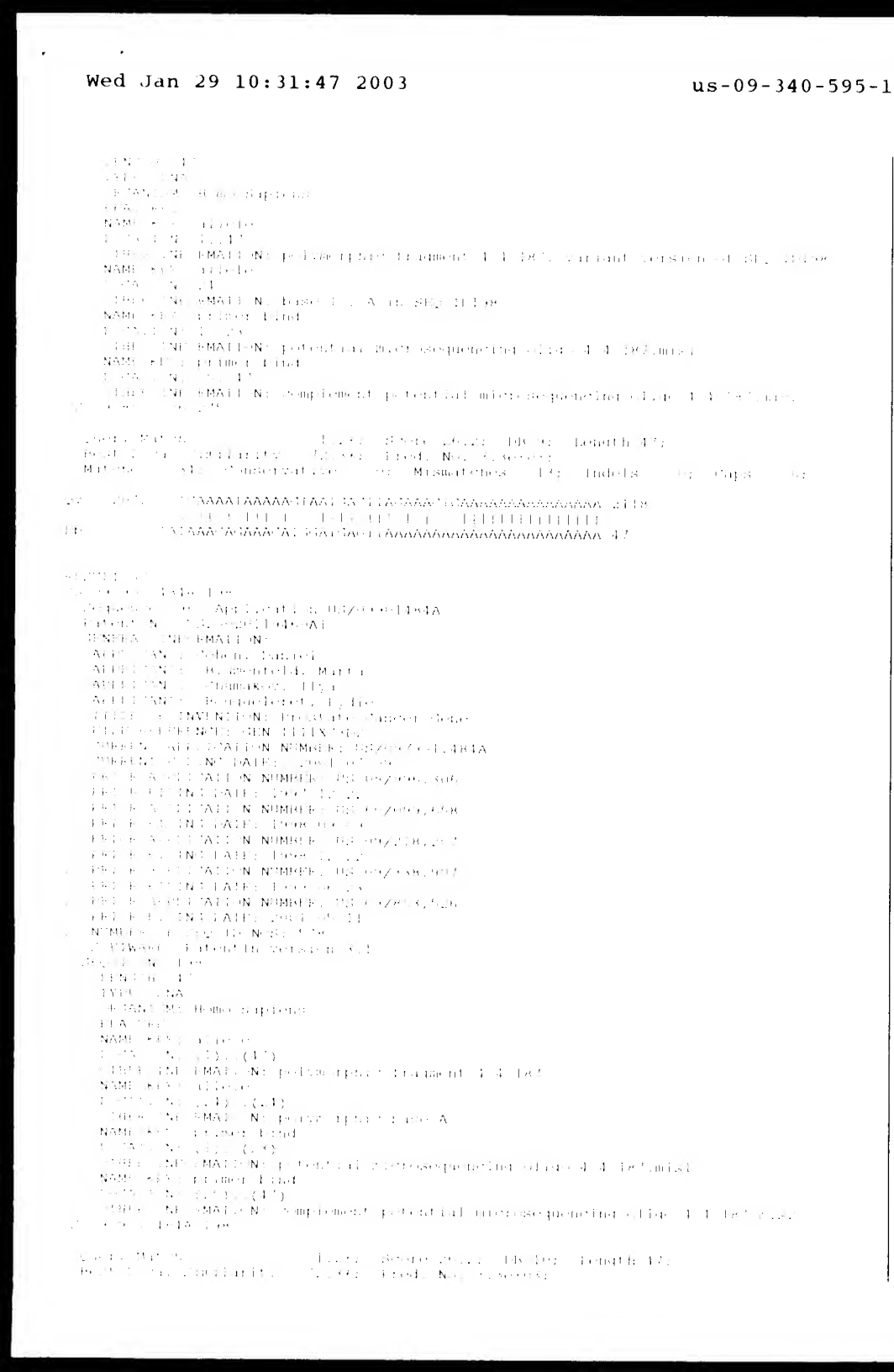

; TITLE OF INVENTION: [illegible] DISEASES OF THE EYE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/[illegible]
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: [illegible]
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/938-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-092-296-1

Query Match 1.2%; Score 25; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2128 AAAAAAAAAAAAAAAAAAAAAAAAA 2104
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Db 29 AAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 4
US-09-923-246-39
; Sequence 39, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: Nelsen, Julia E.
; APPLICANT: Braxell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Cross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/60/222,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/60/213,043
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/60/212,213
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn for Windows Version 3.0

; SEQ ID NO 39
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: [illegible]
US-09-923-246-39

Query Match [illegible]
Best Local Similarity [illegible]
Matches 26; Conservative [illegible]

Qy 2104 GAAAAAAAAAAAAAAAAAAAAAAAAA 2130
[illegible]
Db 26 [illegible] 1

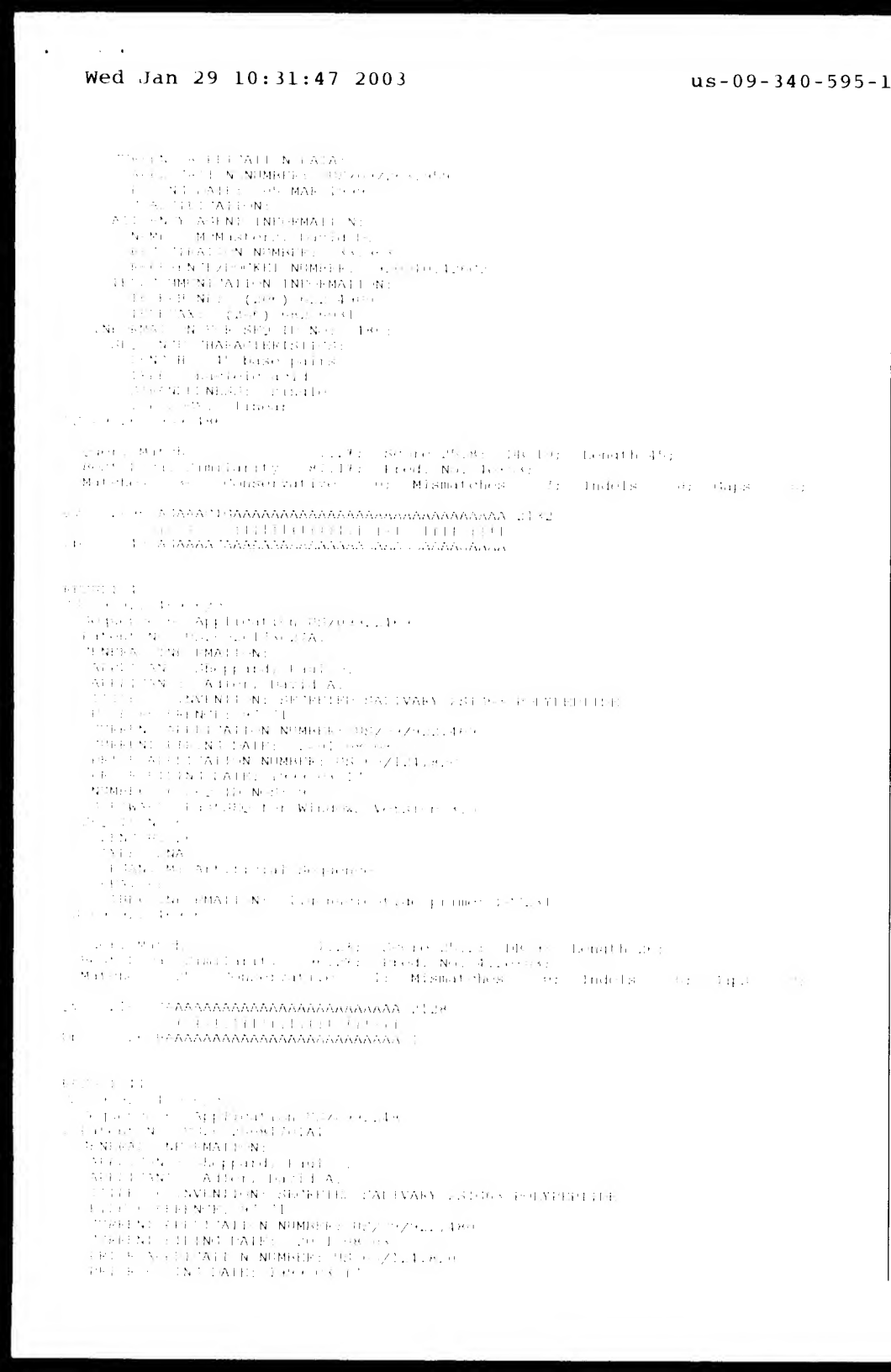
RESULT 41
US-09-923-312-3
; Sequence 3, Application US/09923312
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Lin, Shili
; APPLICANT: Davis, Dean M.
; APPLICANT: Wiedmann, Barbara M.
; TITLE OF INVENTION: GENE SILENCING USING DNA/RNA HYBRIDS
; FILE REFERENCE: 13761-7024
; CURRENT APPLICATION NUMBER: US/09/923,312
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,177
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn for Windows Version 3.1
; SEQ ID NO 3
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Poly(dT) 29mer primer
US-09-920-342-3

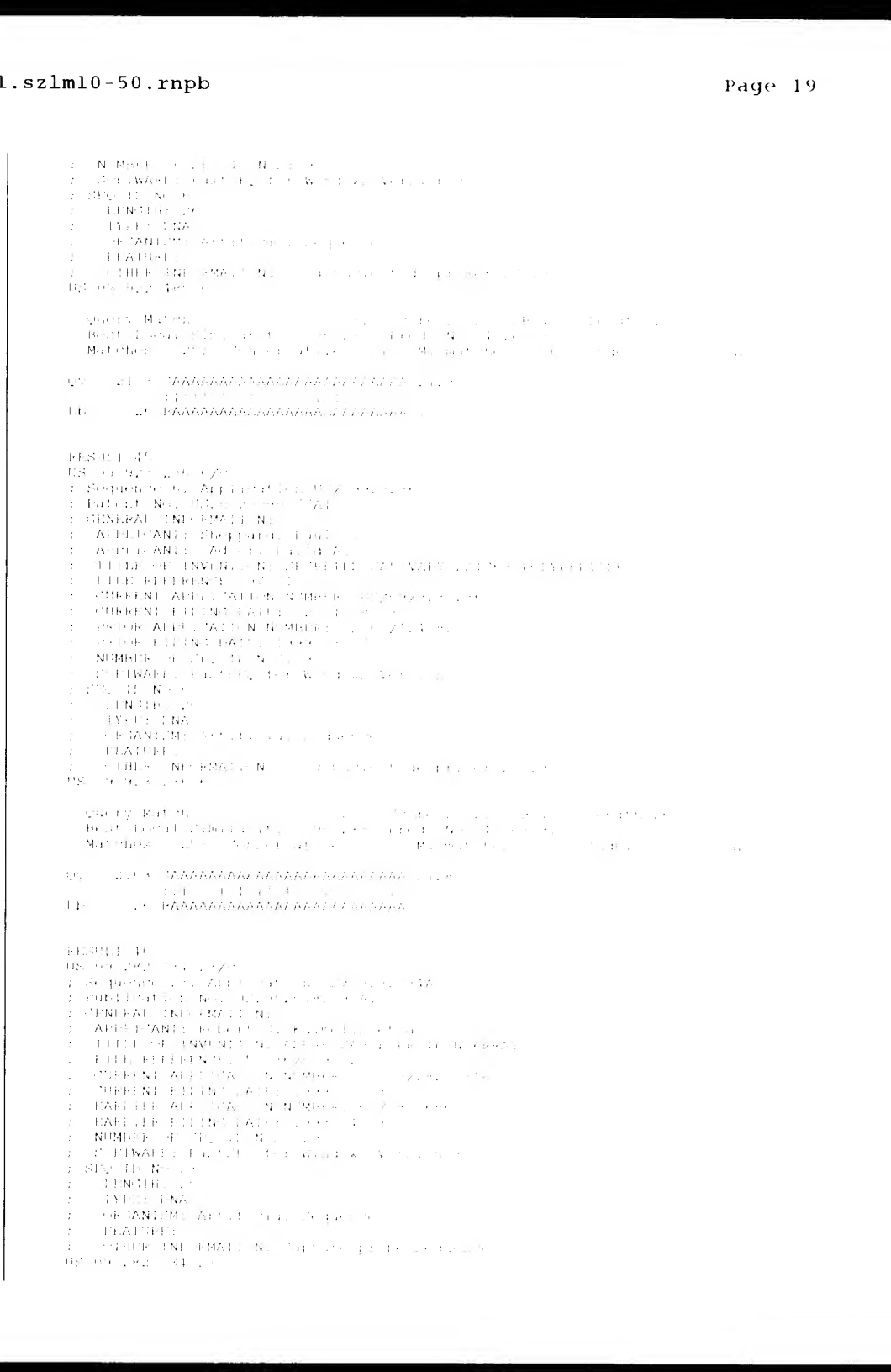
Query Match [illegible]
Best Local Similarity [illegible]
Matches 25; Conservative [illegible]

Qy 2104 AAAAAAAAAAAAAAAAAAAAAAAAA 2080
[illegible]
Db 29 [illegible] 5

RESULT 42
US-09-923-246-39
; Sequence 39, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: Nelsen, Julia E.
; APPLICANT: Braxell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Cross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/60/222,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/60/213,043
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/60/212,213
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn for Windows Version 3.0

RESULT 43
US-09-[illegible]
; Sequence 489, Application US/09[illegible]
; Patent No. US20020[illegible]
; GENERAL INFORMATION:
; APPLICANT: Bond, [illegible]
; APPLICANT: Brown, [illegible]
; APPLICANT: Kuo, Calvin
; TITLE OF INVENTION: HUMAN CYTOKINE AND CYTOKINE RECEPTOR NUCLEIC ACIDS AND METHODS
; NUMBER OF SEQUENCES: 1[illegible]
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version 1.30





Query Match 1.2%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Prod. No. 4.7e-03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2107 AAAAAAAAAAAAAAAAAAAAAAAAA 2131
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Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 47
US-09-922-460-7/c
; Sequence 7, Application US/09922460
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY GENES AND PROTEINS
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,460
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/134,424
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer Z07764a
US-09-922-460-7

Query Match 1.2%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Prod. No. 4.7e-03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2107 AAAAAAAAAAAAAAAAAAAAAAAAA 2131
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Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 48
US-09-922-460-14/c
; Sequence 14, Application US/09922460
; Patent No. US20020018990A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: CHEN, MAOTIAN
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FELDMAN, PAULA M.
; APPLICANT: GUO-N, JULIAN
; APPLICANT: JEANGUENAT, DENISE M.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRAFCHVIL, JAN D.
; APPLICANT: RUSSELL, JOHN T.
; APPLICANT: SCHEFFEL, CHRISTI
; APPLICANT: STROUPE, STEPHEN D.
; APPLICANT: YU, HONG
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASE IN THE LIVER
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,460
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/134,424
; FILING DATE: 17-MAY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Booker, Cheryl L.
; REGISTRATION NUMBER: 37,111
; REFERENCE/DOCKET NUMBER: A120.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/938-2762
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-099-923-14

Query Match 1.2%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Prod. No. 4.7e-03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2107 AAAAAAAAAAAAAAAAAAAAAAAAA 2131
||||||||||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 49
US-09-922-460-7/c
; Sequence 7, Application US/09922460
; Patent No. US20020018990A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY GENES AND PROTEINS
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,460
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/134,424
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer Z07764a
US-09-922-460-7

Query Match 1.2%; Score 25; DB 10; Length 26;
Best Local Similarity 100.0%; Prod. No. 4.7e-03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2107 AAAAAAAAAAAAAAAAAAAAAAAAA 2131
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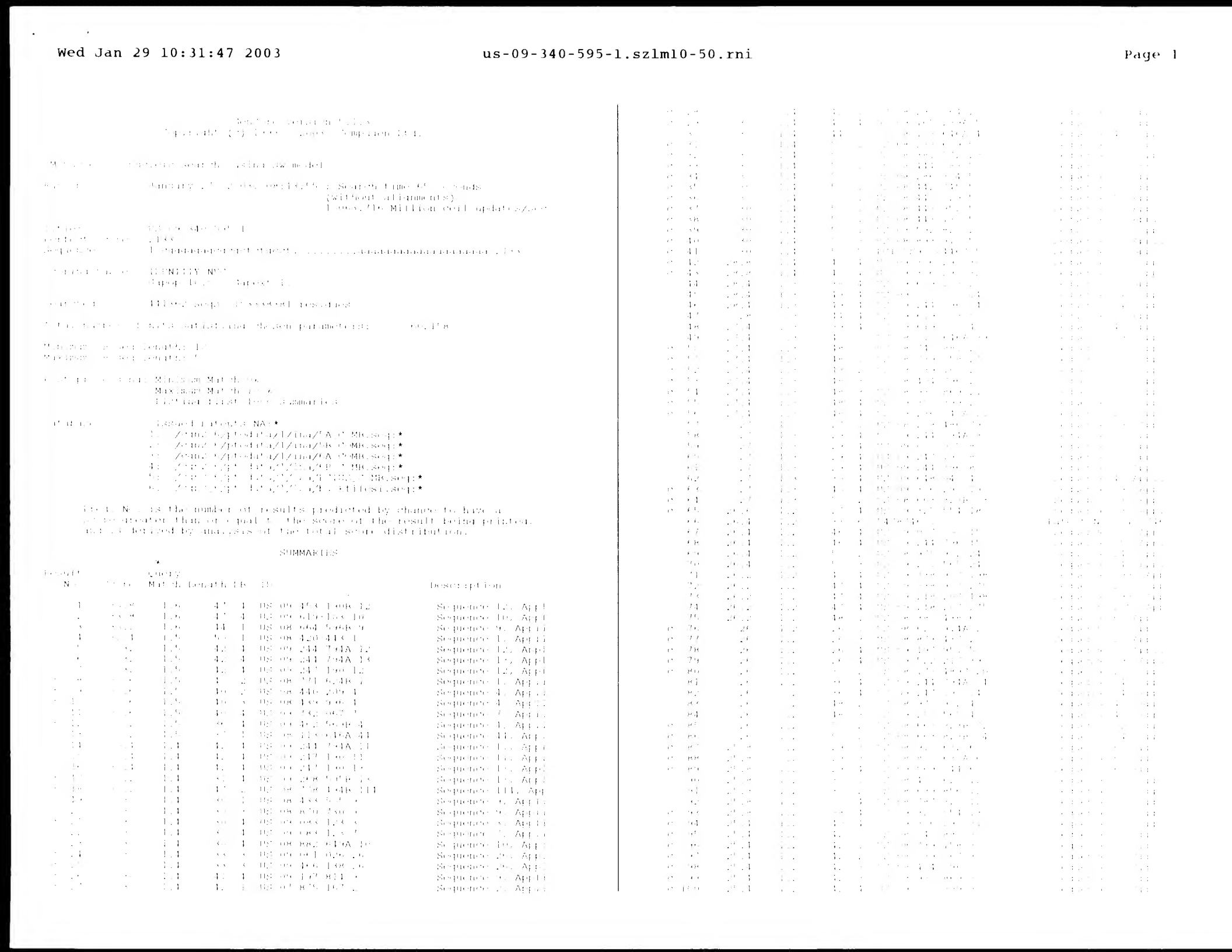
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 50
US-09-923-236-7/c
; Sequence 7, Application US/09923236
; Patent No. US20020068078A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY GENES AND PROTEINS



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c	105	25.2	1.2	26	1	US-09-167-514-10
c	106	25.2	1.2	35	2	US 09 174 489C 19
c	107	25.2	1.2	42	4	US 09 536 936 9
c	108	25	1.2	25	1	US-08-341-148-2
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c	111	25	1.2	25	5	US 09 183 619 5
c	112	25	1.2	25	5	PCT US94 14096 2
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c	115	25	1.2	26	4	US-09-522 217 20
c	116	25	1.2	26	4	US 09 527 345 7
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c	118	25	1.2	38	4	US-09-325 554 8
	119	25	1.2	40	2	US-08 771 621E-20
c	120	25	1.2	40	4	US-09-306 290 12
c	121	24.8	1.2	36	1	US-08-004-800-18
c	122	24.8	1.2	26	1	US 08 412 812 18
c	123	24.8	1.2	36	2	US-08 467-016 18
	124	24.8	1.2	46	2	US-09 307 339 18
c	125	24.6	1.2	47	3	US-08-999-733-6
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	127	24.4	1.1	37	1	US 07 915 215 1
c	128	24.4	1.1	40	4	US 09 306 290 35
c	129	24.4	1.1	40	4	US 09 536 936 8
c	130	24.2	1.1	38	4	US 09 325 554 9
c	131	24.2	1.1	39	4	US-09-325 554 12
c	132	24.2	1.1	39	4	US 09 325 554 14
c	133	24.2	1.1	40	4	US-09-306-290-2
	134	24	1.1	24	1	US 08 611-913A 25
	135	24	1.1	24	1	US-08-486-421-50
	136	24	1.1	24	1	US-08 478 911 50
	137	24	1.1	24	2	US 08-735-381-1
	138	24	1.1	24	2	US-08-486-809-50
	139	24	1.1	24	3	US-09-183 619 7
	140	24	1.1	24	3	US-09-201-674-1
	141	24	1.1	24	4	US-09-536-936-11
	142	24	1.1	24	4	US-09-025-639 4
	143	24	1.1	24	4	US 09 340 237 4
	144	24	1.1	24	4	US 09 742 067 1
	145	24	1.1	32	4	US 09 619 102 14
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c	147	24	1.1	38	4	US 09 325 554 6
c	148	24	1.1	40	4	US 09-306 290 10
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c	151	23.6	1.1	32	1	US 08 126 591 8
c	152	23.6	1.1	32	1	US-08-465-811A-8
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c	154	23.6	1.1	36	1	US-08-004-800-16
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c	156	23.6	1.1	36	2	US 08 167 146 16
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c	160	23.6	1.1	45	5	PCT US93-04256-6
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	162	23.4	1.1	26	3	US-08 910 632 5
	163	23.4	1.1	26	3	US-08-805 631A 5
	164	23.4	1.1	26	4	US-09-569 441 5
c	165	23.4	1.1	32	1	US 07 915 215 2
	166	23.4	1.1	37	1	US-08 113 646A 38
	167	23.4	1.1	43	4	US-09-007-005-16
	168	23.4	1.1	43	4	US 09 244 796 16
c	169	23.4	1.1	44	4	US 09 293 762 2
c	170	23.4	1.1	46	1	US 07 915 215 3
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c	172	23.2	1.1	40	4	US-09-306-290-9
c	173	23	1.1	30	1	US 08 771 781 2
	174	23	1.1	34	4	US 08 211 744A-15
c	175	23	1.1	39	4	US 09 247 290 15
c	176	23	1.1	43	1	US 08 113 646A-24
c	177	23	1.1	43	2	US 08 113 646A-24
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c	180	23	1.1	40	4	US 09 306 290 29
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c	186	22.8	1.1	43	1	US 08 611 913A 33
c	187	22.8	1.1	43	1	US 08 021 730-10
c	188	22.8	1.1	43	1	US 09 306-290-11
c	189	22.8	1.1	43	4	US 09 306 290 34
c	190	22.8	1.1	43	4	US 09 306 290-1
c	191	22.8	1.1	45	1	US 08 113 646-1
c	192	22.6	1.1	29	1	US 08-420 443 2
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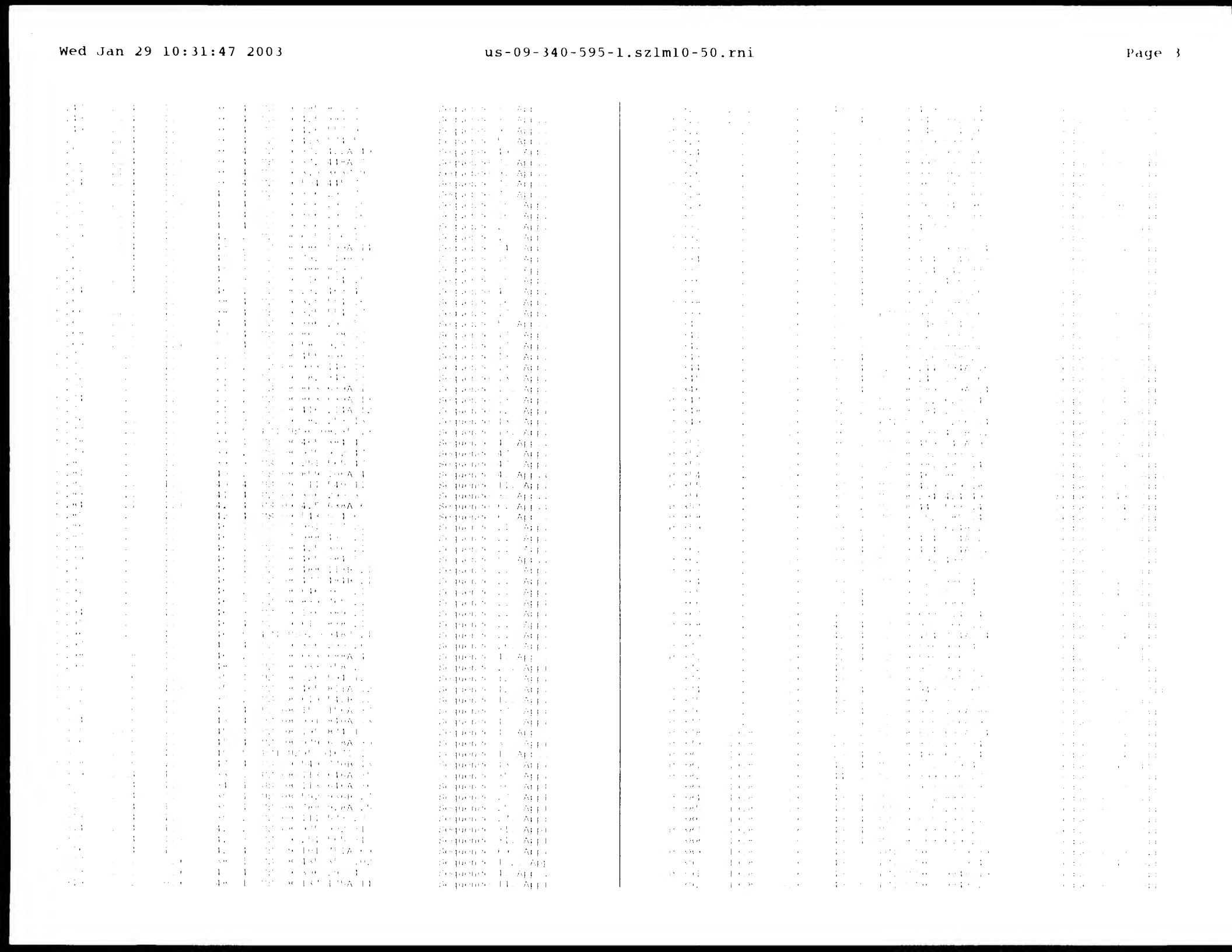
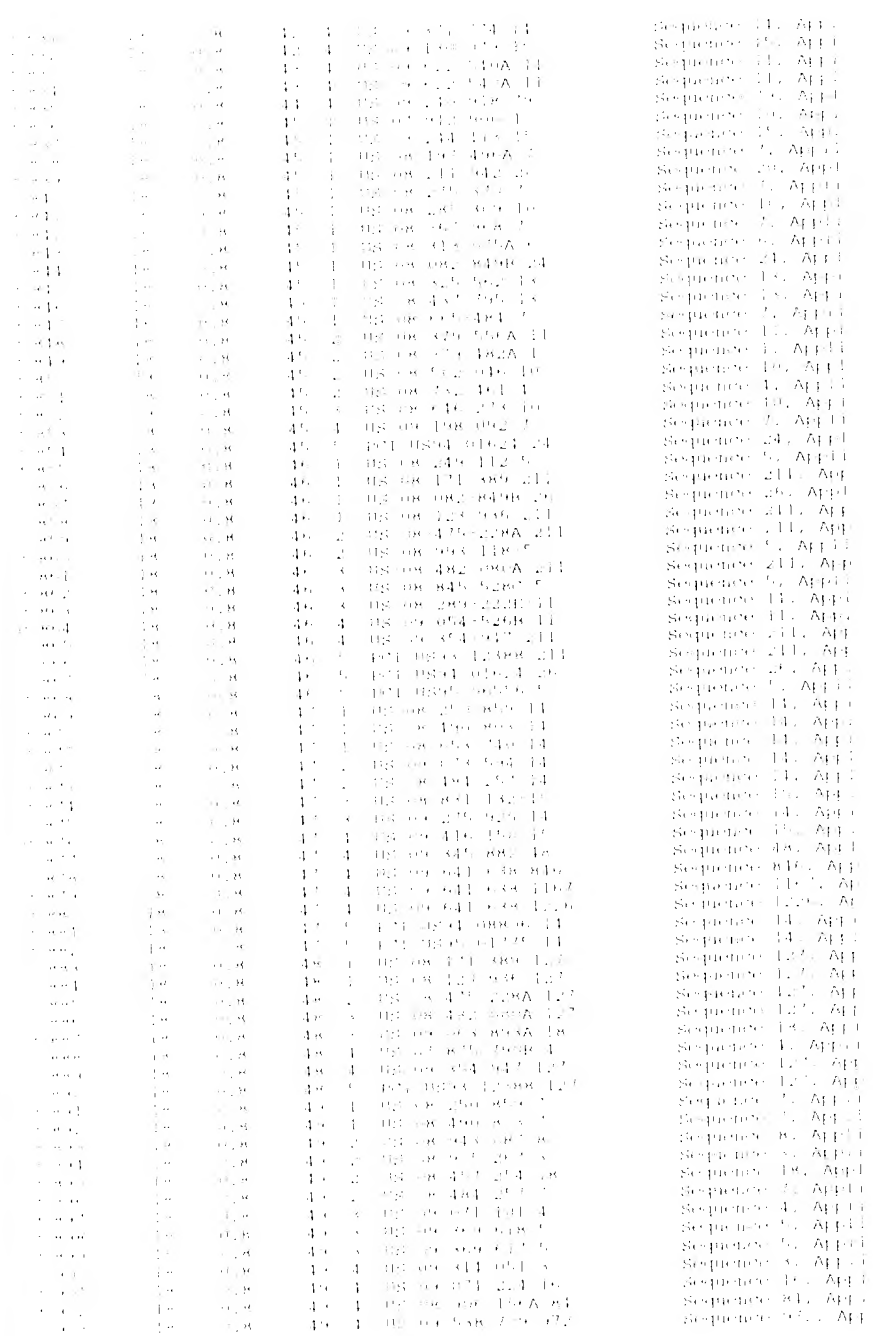
c	195	22.6	1.1	37	4	US-08 465-712-12
c	196	22.6	1.1	37	4	US-09-552-744-12
c	197	22.6	1.1	38	1	US 08 471 7 1A 2
c	198	22.6	1.1	38	4	US-09-325-554-15
c	199	22.6	1.1	41	4	US 09 306 290 35
c	200	22.6	1.1	41	4	US 09 306 290-10
c	201	22.6	1.1	42	2	US 08 461 777A-11
c	202	22.6	1.1	42	2	US 08-477-459-11
c	203	22.6	1.1	42	4	US-08-471-869-11
c	204	22.6	1.1	42	4	US 08 436-411 11
c	205	22.6	1.1	42	5	PCT-US94-01826A-11
c	206	22.6	1.1	42	5	PCT US94 02202A-11
c	207	22.6	1.1	46	1	US 08 08 222 177A 46
	208	22.6	1.1	47	2	US-08-850-049-104
	209	22.6	1.1	47	2	US 08-959 179 104
	210	22.6	1.1	47	4	US-09-414-117-104
	211	22.6	1.1	47	4	US 09 478 117 104
c	212	22.4	1.1	27	1	US 08 113 646A 42
c	213	22.4	1.1	36	1	US 08 113 646A 43
c	214	22.4	1.1	43	4	US 09 306 290 9
c	215	22.4	1.1	43	4	US 09 306-290-21
c	216	22.4	1.1	43	4	US 09 306-290-24
c	217	22.4	1.1	43	4	US 09 306-290-25
c	218	22.4	1.1	43	4	US 09 306 290 1
c	219	22.2	1.0	43	4	US 09 306 290 14
c	220	22.2	1.0	43	1	US-09-306-290-27
c	221	22.2	1.0	44	4	US 09 306 290 37
	222	22	1.0	22	1	US 08 113 646A 1
	223	22	1.0	22	1	US 08 471-050-19
	224	22	1.0	22	4	US 08 347 611A 34
	225	22	1.0	22	4	US-08-959-179-19
c	226	22	1.0	38	1	US 09 325-554-10
c	227	22	1.0	40	4	US 09 306 290 6
c	228	22	1.0	41	1	US 08 113 646A 44
c	229	22	1.0	43	1	US 08 113 646A 44
	230	22	1.0	45	2	US 08 771 781 2
c	231	22	1.0	47	1	US 08 251 665 11
c	232	22	1.0	36	2	US 08-370-441-8
c	233	22	1.0	44	2	US 08 324-002-7
c	234	21.8	1.0	43	4	US 09 306 290 17
c	235	21.8	1.0	43	4	US 09 306 290 22
c	236	21.8	1.0	47	4	US-09-641-638-11B1
	237	21.6	1.0	32	2	US 08 08 [illegible] 38-14
	238	21.6	1.0	32	2	US 08 08 [illegible] 75A-14
c	239	21.6	1.0	43	4	US 09 306 290 28
c	240	21.6	1.0	48	4	US-09-549-770A-14
	241	21.4	1.0	24	1	US-09-164-249B-6
	242	21.4	1.0	37	1	US 08 611 944A-47
c	243	21.4	1.0	37	1	US 08 08 435 [illegible]-118
	244	21.4	1.0	38	1	US 09 392 [illegible]
	245	21.4	1.0	38	1	US-09-358-580-13
	246	21.4	1.0	38	1	US 08 [illegible] 58





977	17.8	0.8	46	3	US-08-271-888A-98	Sequence 98, Appl
978	17.8	0.8	46	3	US-08-747-332-5	Sequence 5, Appli
979	17.8	0.8	46	2	US-08-910-408-98	Sequence 98, Appl
980	17.8	0.8	46	3	US-09-135-418-5	Sequence 5, Appli
981	17.8	0.8	46	3	US-09-249-215-98	Sequence 98, Appl
982	17.8	0.8	47	2	US-09-697-255A-19	Sequence 19, Appl
983	17.8	0.8	47	4	US-09-838-867-238	Sequence 238, App
984	17.8	0.8	47	4	US-09-218-207-238	Sequence 238, App
985	17.8	0.8	47	4	US-09-487-967-19	Sequence 19, Appl
986	17.8	0.8	47	4	US-09-641-638-886	Sequence 886, App
987	17.8	0.8	47	4	US-09-641-638-1031	Sequence 1031, Ap
988	17.8	0.8	48	1	US-07-720-222-45	Sequence 45, Appl
989	17.8	0.8	48	1	US-08-290-301-85	Sequence 85, Appl
990	17.8	0.8	48	4	US-09-013-598-85	Sequence 85, Appl
991	17.8	0.8	49	4	US-08-630-052-27	Sequence 27, Appl
992	17.8	0.9	50	1	US-08-207-981-26	Sequence 26, Appl
993	17.8	0.9	50	1	US-08-983-687-5	Sequence 5, Appli
994	17.8	0.8	50	4	US-08-983-457-42	Sequence 42, Appl
995	17.8	0.8	50	4	US-09-248-356-5	Sequence 5, Appli
996	17.8	0.8	27	4	US-08-548-578-197	Sequence 197, App
997	17.8	1.8	30	1	US-07-982-744B-4	Sequence 4, Appl
998	17.8	1.8	30	3	US-08-612-973-17	Sequence 17, Appl
999	17.8	1.8	30	4	US-08-927-592-17	Sequence 17, Appl
1000	17.8	0.9	31	1	US-08-277-231A-6	Sequence 6, Appl

ALIGNMENTS

```
RESULT 1
US-08-664-596-12
; Sequence 12, Application US/08664596
; Patent No. 6416950
; GENERAL INFORMATION:
;  APPLICANT: Lohse, Peter
;  APPLICANT: Kurz, Markus
;  APPLICANT: Wagner, Richard
;  TITLE OF INVENTION: DNA PROTEIN FUSIONS AND USES THEREOF
;  FILE REFERENCE: 5036/020002
;  CURRENT APPLICATION NUMBER: US/09/459,599
;  CURRENT FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: 60/110,549
;  PRIOR FILING DATE: 1998-12-02
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn for Windows Version 1.0
; SEQ ID NO 12
;  LENGTH: 47
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: DNA linker
US-08-664-596B-12

  Query Match             1.6%;  Score 13.8;  DB 4;  Length 47;
  Best Local Similarity   94.6%;  Pred. No. 8.2;
  Matches   45;  Conservative    ;  Mismatches    2;  Indels    1;  Gaps    1;

Qy    20 AGAAAGTGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2152
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Db     6 AGAAAGTGATAAAAAAAAAAAAAAAAAAAAAAAAAAAA 45


RESULT 2
US-08-664-596-13
; Sequence 13, Application US/08664596
; Patent No. 6429300
; GENERAL INFORMATION:
;  APPLICANT: Kurz, Markus
;  APPLICANT: Lohse, Peter
;  APPLICANT: Wagner, Richard
;  TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;  FILE REFERENCE: 5036/020002
;  CURRENT APPLICATION NUMBER: US/09/459,599
;  CURRENT FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: 60/110,549
;  PRIOR FILING DATE: 1998-12-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn for Windows Version 1.0
; SEQ ID NO 13
;  LENGTH: 47
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: sequence described as an acid linker
US-09-619-104-10

  Query Match             1.6%;  Score 13.8;  DB 4;  Length 47;
  Best Local Similarity   94.6%;  Pred. No. 8.2;
  Matches   45;  Conservative    ;  Mismatches    2;  Indels    1;  Gaps    1;

Qy    20 AGAAAGTGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2152
           ||| | ||| |||||||||||||||||||||||||||
Db     6 AGAAAGTGATAAAAAAAAAAAAAAAAAAAAAAAAAAAA 45


RESULT 3
US-08-664-596B-9
; Sequence 9, Application US/08664596
; Patent No. 5968750
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Scott
;  APPLICANT: McCoy, John
;  APPLICANT: LaVallie, Edward
;  APPLICANT: Rucker, Lisa
;  APPLICANT: Merberg, David
;  APPLICANT: Treacy, Maria
;  APPLICANT: Evans, Cheryl
;  APPLICANT: Spaltman, Vikki
;  APPLICANT: Edwards, Michael
;  TITLE OF INVENTION: GENERIC PROTEIN AND POLYNUCLEOTIDES
;  TITLE OF INVENTION: EXPRESSION SYSTEM
;  NUMBER OF SEQUENCES: 27
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Genetics Institute, Inc.
;    STREET: 87 Cambridge Park Drive
;    CITY: Cambridge
;    STATE: Massachusetts
;    COUNTRY: U.S.A.
;    ZIP: 02140
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: FastSEQ for Windows Version 1.0
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/664,596B
;    FILING DATE:
;    CLASSIFICATION: 514
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Brown, Scott A.
;    REGISTRATION NUMBER: 42,712
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (617) 876-8181
;    TELEFAX: (617) 876-5851
;  INFORMATION FOR SEQ ID NO: 9
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 44 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;    MOLECULE TYPE: cDNA
US-08-664-596B-9

  Query Match             1.6%;  Score 13.8;  DB 4;  Length 44;
  Best Local Similarity   94.6%;  Pred. No. 8.2;
  Matches   45;  Conservative    ;  Mismatches    2;  Indels    1;  Gaps    1;
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;  PRIOR APPLICATION NUMBER: 08/559,247,149
;  CURRENT FILING DATE: 1999-02-09
;  EARLIER APPLICATION NUMBER: 08/035,963
;  EARLIER FILING DATE: 1997-03-21
;  EARLIER APPLICATION NUMBER: 08/004,191
;  EARLIER FILING DATE: 1997-11-06
;  EARLIER APPLICATION NUMBER: 08/997,005
;  EARLIER FILING DATE: 1998-01-14
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 12
;    LENGTH: 42
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Translation template
RS  <_247-196-12

  Query Match                 1.5%;  Score 32;  DB 4;  Length 42;
  Best Local Similarity   96.9%;  Pred. No. 22;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     20 GAUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 53
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Db      9 AACGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40


RESULT 6
US-08-771-624B-1/c
; Sequence 1, Application US/08771624B
; Patent No. 5914240
;  GENERAL INFORMATION:
;    APPLICANT:  Lin, Yen Ping
;    APPLICANT:  Patel, Rajesh D.
;    APPLICANT:  Korn, Norith
;    APPLICANT:  Lin, Claire
;    APPLICANT:  Rose, Samuel J.
;    APPLICANT:  Ullman, Edwin F.
;    TITLE OF INVENTION:  Homogeneous Amplification and Detection
;    TITLE OF INVENTION:  of Nucleic Acids
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Boehring Diagnostics GmbH, c/o Dade Behring Inc.
;      STREET:  1717 Deerfield Road
;      CITY:  Deerfield
;      STATE:  Illinois
;      COUNTRY:  US
;      ZIP:  60015-0778
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/771,624B
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/559,247
;      FILING DATE:  22-DEC-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pezzuto, Lois E.
;      REGISTRATION NUMBER:  39,974
;      REFERENCE/DOCKET NUMBER:  1930
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (847) 267-5364
;      TELEFAX:  (847) 267-5024
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-771-624B-1

  Query Match                 1.5%;  Score 32;  DB 4;  Length 40;
  Best Local Similarity   96.9%;  Pred. No. 22;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     20 GAUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 53
          | | | ||||||||||||||||||||||||||||||||||
Db      7 AAUGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40


RESULT 9
US-08-440-209A-4/c
; Sequence 4, Application US/08440209A
; Patent No. 5928857
;  GENERAL INFORMATION:
;    APPLICANT:  Ban, Jamal D.
;    APPLICANT:  Spector, Deborah P.
;    TITLE OF INVENTION:  Methods and Compositions for Detecting Viral
;    TITLE OF INVENTION:  Diseases Caused by Viroids
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/440,209A
;      FILING DATE:  12-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/277,905
;      FILING DATE:  20-JUN-1994
;      APPLICATION NUMBER:  US 08/162,565
;      FILING DATE:  06-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gallik, Anthony
;      REGISTRATION NUMBER:  37,886
;      REFERENCE/DOCKET NUMBER:  0112/
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 720-3500
;      TELEFAX:  617 720-2441
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-440-209A-4

  Query Match                 1.5%;  Score 32;  DB 4;  Length 40;
  Best Local Similarity   96.9%;  Pred. No. 22;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     20 GAUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 53
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Db      7 AAUGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40
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; ZIP: 22201 4714
; MACHINE READABLE DATA:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/113,646A
; FILING DATE: 31 AUG 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/084,403
; FILING DATE: 10-AUG-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1079-20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 248727 NIXN UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US 08/113,646A-44

Query Match 1.5%; Score 1.2; DB 1; Length 37;
Best Local Similarity 91.7%; Pred. No. 33;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAUUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2112
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Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47

RESULT 14
US-09-244-794A-11
; Sequence 11, Application US/09244794A
; Patent No. 6214553
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF RNA-FOLDS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/244,794A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/036,962
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 60/064,191
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 60/067,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 42
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US 09/244,794A 11

Query Match 1.4%; Score 90.4; DB 4; Length 42;
Best Local Similarity 91.8%; Pred. No. 52;
Matches 45; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2099 AACUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2143
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Db 1 AACUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 42

RESULT 15
US-09-247-190-11
; Sequence 11, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF RNA-PROTEIN FUSIONS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/247,190
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/036,962
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,191
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/067,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 42
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-247-190-11

Query Match 1.4%; Score 90.4; DB 4; Length 42;
Best Local Similarity 91.8%; Pred. No. 52;
Matches 45; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2099 AACUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2143
||| |||||||||||||||||||||||||||||||||||
Db 1 AACUUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 42

RESULT 16
US-09-247-190-13
; Sequence 13, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF RNA-PROTEIN FUSIONS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/247,190
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/036,962
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,191
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/067,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 42
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-247-190-13

Query Match 1.4%; Score 90.4; DB 4; Length 42;
Best Local Similarity 91.8%; Pred. No. 52;

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  Matches    96;  Conservative     0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2106 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2135
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Db       1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30


RESULT 2
US-08-083-123-7
; Sequence 7, Application US/08083123
; Patent No. 6017707
; GENERAL INFORMATION:
;   APPLICANT:  MANDRAND, Bernard
;   APPLICANT:  CROS, Philippe
;   APPLICANT:  DELAIR, Thierry
;   APPLICANT:  CHARLES, Marie-Helene
;   APPLICANT:  ENGUT, Marie Nx. 6017707lle
;   APPLICANT:  PINPET, Christian
;   TITLE OF INVENTION:  REAGENT AND METHOD FOR THE DETECTION OF
;   TITLE OF INVENTION:  X-RAY DIFFRACTION STUDY AND MODEL BUILDING
;   NUMBER OF SEQUENCES:  11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  GLIFT & BERRIDGE, PLC
;     STREET:  P.O. Box 19928
;     CITY:  Alexandria
;     STATE:  VA
;     COUNTRY:  USA
;     ZIP:  22320
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/870,2--
;     FILING DATE:  06-JUN-1997
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  BERRIDGE, WILLIAM F.
;     REGISTRATION NUMBER:  36,023
;     REFERENCE/DOCKET NUMBER:  WIS 97-10A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-836-6400
;     TELEFAX:  703 836-2787
;  INFORMATION FOR SEQ ID NO:  7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  60 bases
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA
US-08-083-123-7

  Query Match             1.4%;  Score 96;  DB 8;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   96;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2106 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2135
             ||||||||||||||||||||||||||||||
Db       1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30


RESULT 2
US-09-083-123-7
; Sequence 7, Application US/09083123
; Patent No. 6326148
; GENERAL INFORMATION:
;   APPLICANT: Oram, Hendrik
;   APPLICANT: Seeger, Corina
;   TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
;   TITLE OF INVENTION: Acids
;   FILE REFERENCE: sequence listing
;   CURRENT APPLICATION NUMBER: US/09/083,123
;   CURRENT FILING DATE: 1998-05-22
;   EARLIER APPLICATION NUMBER: EP 97108099.2
;   EARLIER FILING DATE: 1997-05-22
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Made to Order
US-09-083-123-7

  Query Match             1.4%;  Score 96;  DB 8;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   96;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2106 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2135
             ||||||||||||||||||||||||||||||
Db       1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30


RESULT 23
US-08-082-949A-1
; Sequence 1, Application US/08082949A
; Patent No. 5841017
;   GENERAL INFORMATION:
;         APPLICANT: Lockhart, David J.
;                    Chee, Mark
;                    Gunderson, Kevin
;                    Kulp, John L. III
;                    Wolfson, Dana
;                    Trulson, Matthew O.
;                    Lee, Doris
;                    Frank, Bruce M.
;                    Mittmann, Hallie
```
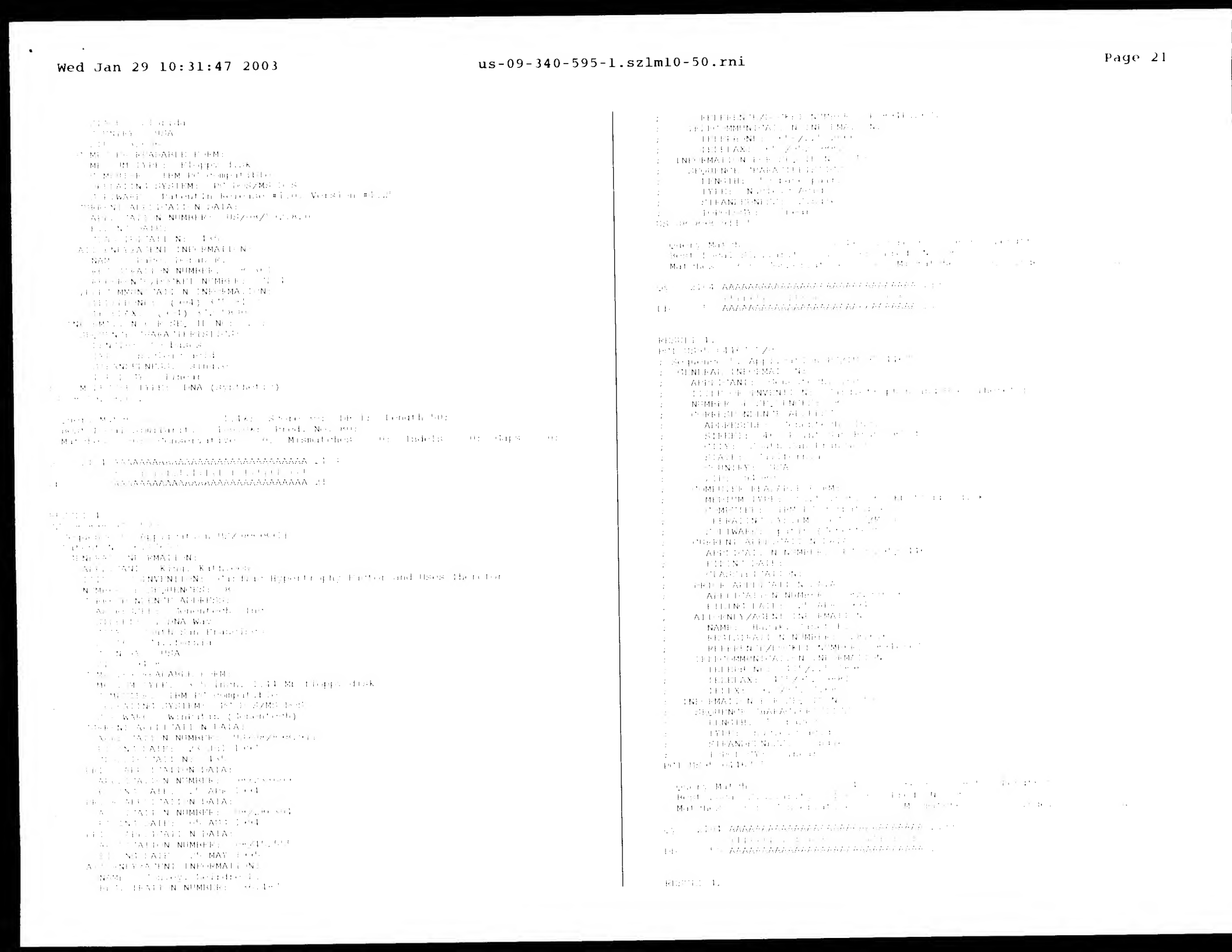

```
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  41 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc= "primer"
US-09-340-138-26

  Query Match                 1.4%;  Score 30;  DB 4;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ATGCATGCATGCATGCATGCATGCATGCAT 31
          ||||||||||||||||||||||||||||||
Db      1 ATGCATGCATGCATGCATGCATGCATGCAT 30


RESULT 29
US-08-614-9/2
; Sequence 9, Application US/08614814A
; Patent No. 5416220
; GENERAL INFORMATION:
;  APPLICANT: Christensen, Love
;  TITLE OF INVENTION: A Transcription Factor
;  FILE REFERENCE: 4484.204-US
;  CURRENT APPLICATION NUMBER: US/08/614,814A
;  CURRENT FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: 0748/96
;  EARLIER FILING DATE: 1996-07-05
;  EARLIER APPLICATION NUMBER: 60/021,850
;  EARLIER FILING DATE: 1997-07-07
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;    LENGTH: 41
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Primer
US-09-147-814-9

  Query Match                 1.4%;  Score 30;  DB 4;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 ATGCATGCATGCATGCATGCATGCATGCAT 50
           ||||||||||||||||||||||||||||||
Db      12 ATGCATGCATGCATGCATGCATGCATGCAT 41


RESULT 30
US-07-875-167-2/2
; Sequence 2, Application US/07875167
; Patent No. 5298584
; GENERAL INFORMATION:
;     APPLICANT:  Ludger Beerhues; Hans-Ulrich Stiegand;
;     APPLICANT:  Herbert Boal; Antonius Lobberding;
;     APPLICANT:  Gerhard Becker; Bruno Bomer; Thomas
;     APPLICANT:  Boeker; Gustav Franke;
;     TITLE OF INVENTION:  PLASMID SYSTEMS AND
;     TITLE OF INVENTION:  PREPARATION AND USE THEREOF
;     NUMBER OF SEQUENCES:  2
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SPRUNG HORN KRAMER & WOODS
;       STREET:  1140 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 5.25 inch, 1.2 MB
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/875,167
;       FILING DATE:  1992-12-
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  P 41 14 642.1 (Germany)
;       FILING DATE:  May 7, 1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kurt G. Briscoe
;       REGISTRATION NUMBER:  [illegible]
;       REFERENCE/DOCKET NUMBER:  Page 951, 870
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 758-3500
;       TELEFAX:  (212) 758-3575
;       TELEX:  42790 SPHP UI
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  42 Nucleotides
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
US-07-875-167-2

  Query Match                 1.4%;  Score 30;  DB 5;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ATGCATGCATGCATGCATGCATGCATGCAT 31
          ||||||||||||||||||||||||||||||
Db      13 ATGCATGCATGCATGCATGCATGCATGCAT 42


RESULT 28
US-08-287-164-2/2
; Sequence 2, Application US/08287164
; Patent No. 5578713
;  GENERAL INFORMATION:
;     APPLICANT:  Dubber, Bettina
;     APPLICANT:  Adorf, Sylvia
;     APPLICANT:  Joachim Probst
;     TITLE OF INVENTION:  Process and Means for Cloning and
;     TITLE OF INVENTION:  Heart Specific Genes and Polymers of Expression and
;     TITLE OF INVENTION:  Their Use in Gene
;     NUMBER OF SEQUENCES:  2
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Connolly and Hutz
;       STREET:  1220 Market Street
;       CITY:  Wilmington
;       STATE:  Delaware
;       COUNTRY:  U.S.A.
;       ZIP:  19899
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" 1.44Mb diskette
;       COMPUTER:  IBM/PC or Compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/287,164
;       FILING DATE:  08-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  G/005,611
;       FILING DATE:  1 JAN 1993
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  42 bases
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  single stranded
;       TOPOLOGY:  linear
US-08-287-164-2
```

```
Qy    2704 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
           ||||||||||||||||||||||||||||||||
Db      61 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


RESULT 52
US-08-431-572-20/c
; Sequence 20, Application US/08431572
; Patent No. 5565340
; GENERAL INFORMATION:
;   APPLICANT: Chernajk, Alex
;   APPLICANT: Shatchenko, Luda
;   APPLICANT: Siebert, Paul
;   APPLICANT: Lukianov, Sergey
;   APPLICANT: Lukianov, Konstantin
;   APPLICANT: Gurskaya, Nadia
;   APPLICANT: Tarabykin, Victor
;   APPLICANT: Scerdiov, Evgeny
;   TITLE OF INVENTION: METHOD FOR DIFFERENTIAL DNA DISPLAY
;   TITLE OF INVENTION: AMPLIFICATION CLONING KIT
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Saliwanchik & Saliwanchik
;     STREET: 2421 N.W. 41st Street, Suite A-1
;     CITY: Gainesville
;     STATE: Florida
;     COUNTRY: USA
;     ZIP: 32606
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/431,572
;     FILING DATE:
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pace, Doran R.
;     REGISTRATION NUMBER: 28,561
;     REFERENCE/DOCKET NUMBER: CB-4
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (904) 375-8100
;     TELEFAX: (904) 372-5800
;  INFORMATION FOR SEQ ID NO: 20:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 50 bases
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (synthetic)
US-08-431-572-20

  Query Match             1.4%;  Score 50;  DB 1;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2743 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2792
           ||||||||||||||||||||||||||||||||||
Db      21 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 70


RESULT 53
US-08-444-083-5/c
; Sequence 5, Application US/08444083
; Patent No. 5571675
; GENERAL INFORMATION:
;   APPLICANT: Baker, Joffre
;   APPLICANT: Chien, Kenneth
;   APPLICANT: King, Kathleen
;   APPLICANT: Pennica, Diane
;   APPLICANT: Wood, William
;   TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Thereof
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET: 460 Point San Bruno Blvd
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: patIn (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/444,083
;     FILING DATE: 19-MAY-1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/245,465
;     FILING DATE: 17-MAY-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/245,465
;     FILING DATE: 17-MAY-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Torchia, Timothy E.
;     REGISTRATION NUMBER: 31,097
;     REFERENCE/DOCKET NUMBER: 1941P05
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415/225-8677
;     TELEFAX: 415/952-9881
;     TELEX: 910/371-7168
;  INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 50 bases
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-444-083-5

  Query Match             1.4%;  Score 50;  DB 1;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2743 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2792
           ||||||||||||||||||||||||||||||||||
Db      21 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 70


RESULT 54
US-08-286-394-5/c
; Sequence 5, Application US/08286394
; Patent No. 5521284
; GENERAL INFORMATION:
;   APPLICANT: Baker, Joffre
;   APPLICANT: Chien, Kenneth
;   APPLICANT: King, Kathleen
;   APPLICANT: Pennica, Diane
;   APPLICANT: Wood, William
;   TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Thereof
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET: 460 Point San Bruno Blvd
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: patIn (Genentech)
```

```
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2594 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2643
           ||||||||||||||||||||||||||||||||||||||||||
Db       50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


RESULT 47
US-08-144-952-5/c
; Sequence 5, Application US/08144952
; Patent No. 5679545
; GENERAL INFORMATION:
;   APPLICANT:  Baker, Jotiro
;   APPLICANT:  Chien, Kenneth
;   APPLICANT:  Kim, Kathleen
;   APPLICANT:  Pennica, Diane
;   APPLICANT:  Wood, William
;   TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Thereto
;   NUMBER OF SEQUENCES:  9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  460 Point San Bruno Blvd
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/144,952
;     FILING DATE:  17-MAY-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/239,079
;     FILING DATE:  25-APR-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/286,424
;     FILING DATE:  05-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Dorcha, Timothy E.
;     REGISTRATION NUMBER:  36,700
;     REFERENCE/DOCKET NUMBER:  P941P1D4
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-9871
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  50 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-144-952-5

  Query Match             1.4%;  Score 35;  DB 1;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2594 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2643
           ||||||||||||||||||||||||||||||||||||||||||
Db       50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


RESULT 48
US-08-144-130-5/c
; Sequence 5, Application US/08144130
; Patent No. 5723585
; GENERAL INFORMATION:
;   APPLICANT:  Baker, Jotiro
;   APPLICANT:  Chien, Kenneth
;   APPLICANT:  Kim, Kathleen
;   APPLICANT:  Pennica, Diane
;   APPLICANT:  Wood, William
;   TITLE OF INVENTION:  Cardiac Hypertrophy Factor and Uses Thereto
;   NUMBER OF SEQUENCES:  9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  460 Point San Bruno Blvd
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/144,952
;     FILING DATE:  17-MAY-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/286,424
;     FILING DATE:  05-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Dorcha, Timothy E.
;     REGISTRATION NUMBER:  36,700
;     REFERENCE/DOCKET NUMBER:  P941P1D4
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-9871
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  50 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-144-130-5

  Query Match             1.4%;  Score 35;  DB 1;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2594 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2643
           ||||||||||||||||||||||||||||||||||||||||||
Db       50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


RESULT 49
US-08-542-820-2/c
; Sequence 20, Application US/08542820
; Patent No. 5756622
; GENERAL INFORMATION:
;   APPLICANT:  Churchill, Alan
;   APPLICANT:  Diamond, Luda
;   APPLICANT:  Siegel, Ira
;   APPLICANT:  Lukiw, Walter
;   APPLICANT:  Lukiw, Krystyna
;   APPLICANT:  Shcherbak, Nadia
;   APPLICANT:  Tarabykin, Vsevolod
;   APPLICANT:  Skoblov, Yuriy
;   TITLE OF INVENTION:  METHOD FOR STIMULATING DNA TREATMENT
;   TITLE OF INVENTION:  AMELIORATION OF NEURONAL DNA
;   NUMBER OF SEQUENCES:  20
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
;     STREET:  2441 N.W. 41st Street, Suite A-1
;     CITY:  Gainesville
```



US-09-340-595-1/c
; Sequence 50, Application US/09340595
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; APPLICANT: Makrigiorgos, George M.
; TITLE OF INVENTION: METHODS FOR SOLID PHASE AMPLIFICATION OF DNA TEMPLATE
; TITLE OF INVENTION: (SPAM) USING MULTIBEADS
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/340,595
; CURRENT FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer pH
; OTHER INFORMATION: RH852
US-09-340-595-50

Query Match 1.4%; Score 28.8; DB 4; Length 40;
Best Local Similarity 82.5%; Prod. No. 1.4e-02;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2033 TTTTTTAAAAATTTAAAAAAAAAAAAAAAAAAAAAAAAA 2125
|||||||||||||||||||||||||||||||||||||||
Db 10 TAAATTAATAAATTAAAAAAAAAAAAAAAAAAAAAAAAA 50

RESULT 44
US-09-340-595-42/c
; Sequence 42, Application US/09340595
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; APPLICANT: Mukhopadhyay, Sunil
; TITLE OF INVENTION: METH OD F OR S OLI D PHAS E AMPLIFI CATI O N O F DNA TEMPLATE
; TITLE OF INVENTION: (SPAM) USING MULTIBEADS
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/340,595
; CURRENT FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer pH
; OTHER INFORMATION: RH854
US-09-340-595-42

Query Match 1.4%; Score 28.8; DB 4; Length 40;
Best Local Similarity 82.5%; Prod. No. 1.4e-02;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2092 ATTTAAAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2183
||| | |||| | ||| ||||||||||||||||||||||
Db 40 ATTCAAATAACATTTTAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 45
US-09-103-103-2
; Sequence 2, Application US/09103103
; Patent No. 6294330
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 5006/0100.2
; CURRENT APPLICATION NUMBER: US/09/103,103
; CURRENT FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/045,934
; PRIOR FILING DATE: 1997-05-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed sequence for use as a linker
US-09-103-103-2

Query Match 1.4%; Score 28.8; DB 4; Length 40;
Best Local Similarity 82.5%; Prod. No. 1.4e-02;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

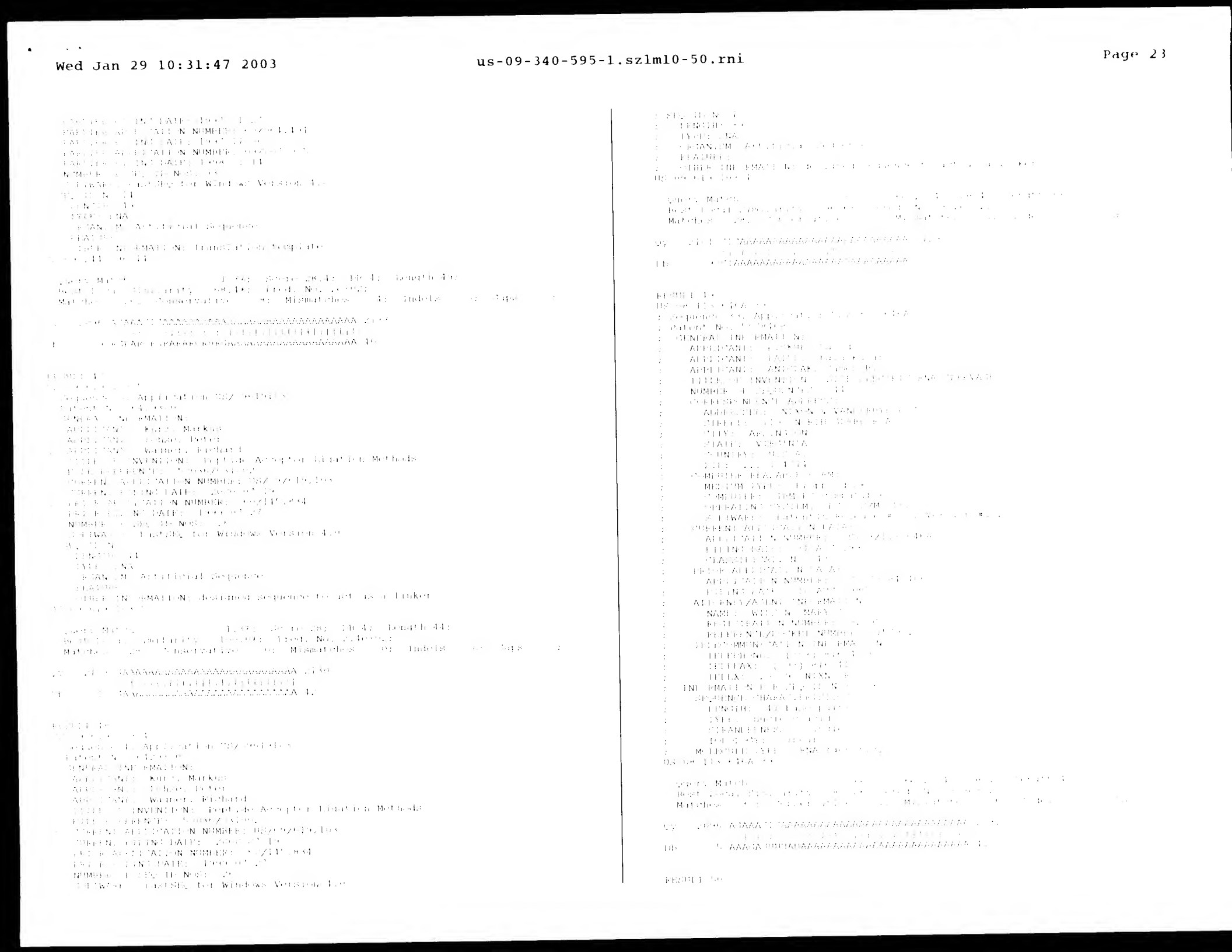
Qy 2092 ATTTAAAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2183
||| | |||| | ||| ||||||||||||||||||||||
Db 40 ATTCAAATAACATTTTAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 46
US-09-007-005-14
; Sequence 14, Application US/09007005
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Sz Stak, Ga Sk W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rito
; TITLE OF INVENTION: SELECTI N O F PEPTI DES USING RNA-PEPTI DE
; TITLE OF INVENTION: FUSI NS
; FILE REFERENCE: 007a/000005
; CURRENT APPLICATION NUMBER: US/09/007,005
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Transcript template
US-09-007-005-14

Query Match 1.4%; Score 28.8; DB 4; Length 49;
Best Local Similarity 82.5%; Prod. No. 2.1e-02;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2092 ATTTAAAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2183
||| | |||| | ||| ||||||||||||||||||||||
Db 9 ATTCAAATAACATTTTAAAAAAAAAAAAAAAAAAAAAAAA 49

RESULT 47
US-09-244-706-11
; Sequence 14, Application US/09244706
; Patent No. 6291431
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rito
; TITLE OF INVENTION: SELECTION OF PEPTIDES USING RNA-PEPTIDE
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 007a/000005
; CURRENT APPLICATION NUMBER: US/09/244,706
; CURRENT FILING DATE: 1999-02-
; EARLIER APPLICATION NUMBER: 60/064,491



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; Sequence 21, Application US/08741881
; Patent No. 5789545
;  GENERAL INFORMATION:
;     APPLICANT:  Butensky Jr, Thomas W
;     APPLICANT:  Polo, John M.
;     APPLICANT:  Ibanez, Carlos E.
;     APPLICANT:  Chang, Stephen M.W.
;     APPLICANT:  Jolly, Douglas J.
;     APPLICANT:  Driver, David A.
;     APPLICANT:  Polli, Barbara A.
;     TITLE OF INVENTION:  HIGHLY EFFICIENT LAYERED VECTOR INITIATION SYSTEMS
;     NUMBER OF SEQUENCES:  128
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SEED and BERRY LLP
;       STREET:  6300 Columbia Center, 701 Fifth Avenue
;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  US
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/741,881
;       FILING DATE:  30-OCT-1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McMasters, David D.
;       REGISTRATION NUMBER:  34,963
;       REFERENCE/DOCKET NUMBER:  9.0-[illegible]/Tibo.007
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  21:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  48 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-741-881-21

  Query Match             1.3%;  Score 27.4;  DB 1;  Length 48;
  Best Local Similarity   88.88%;  Prob. No. 3.6e-02;
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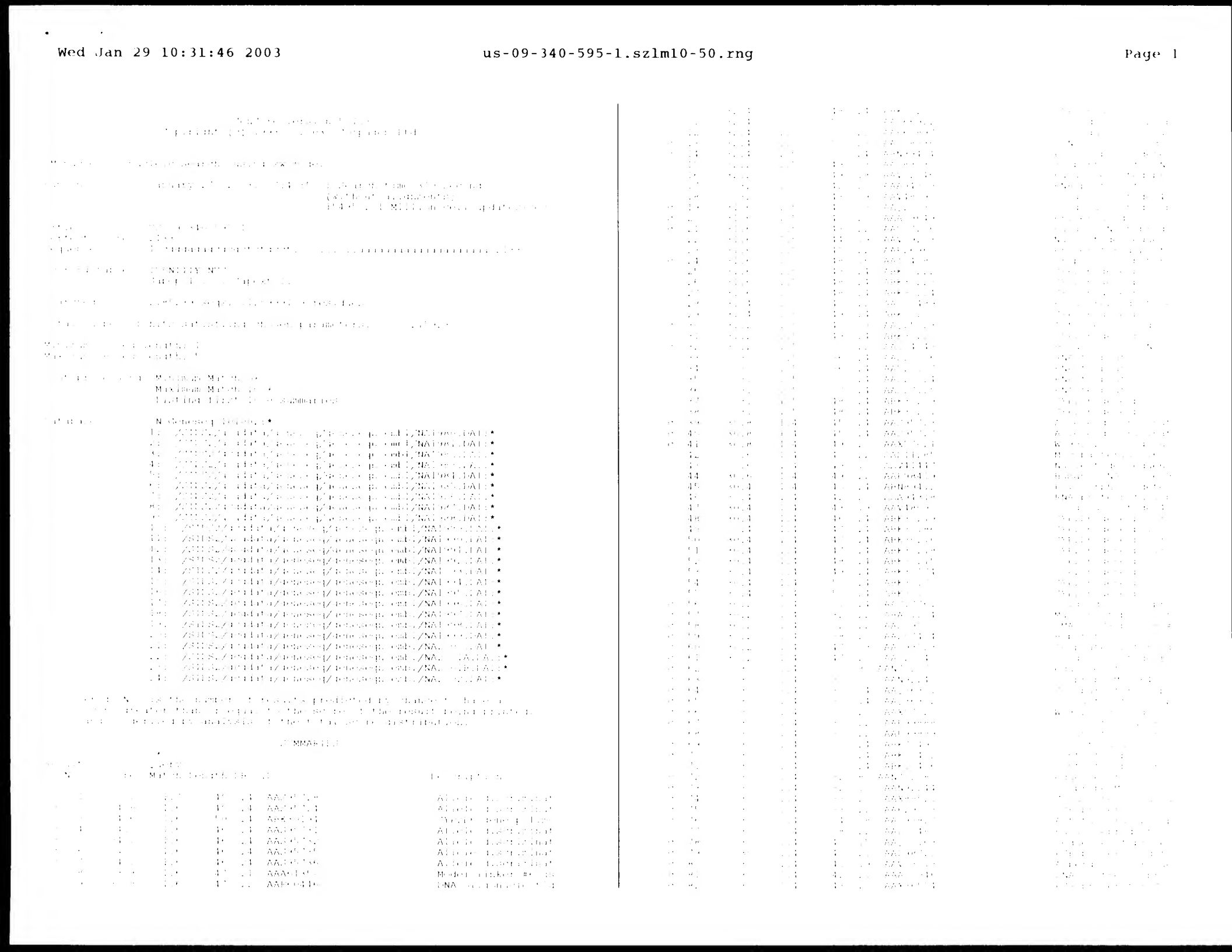

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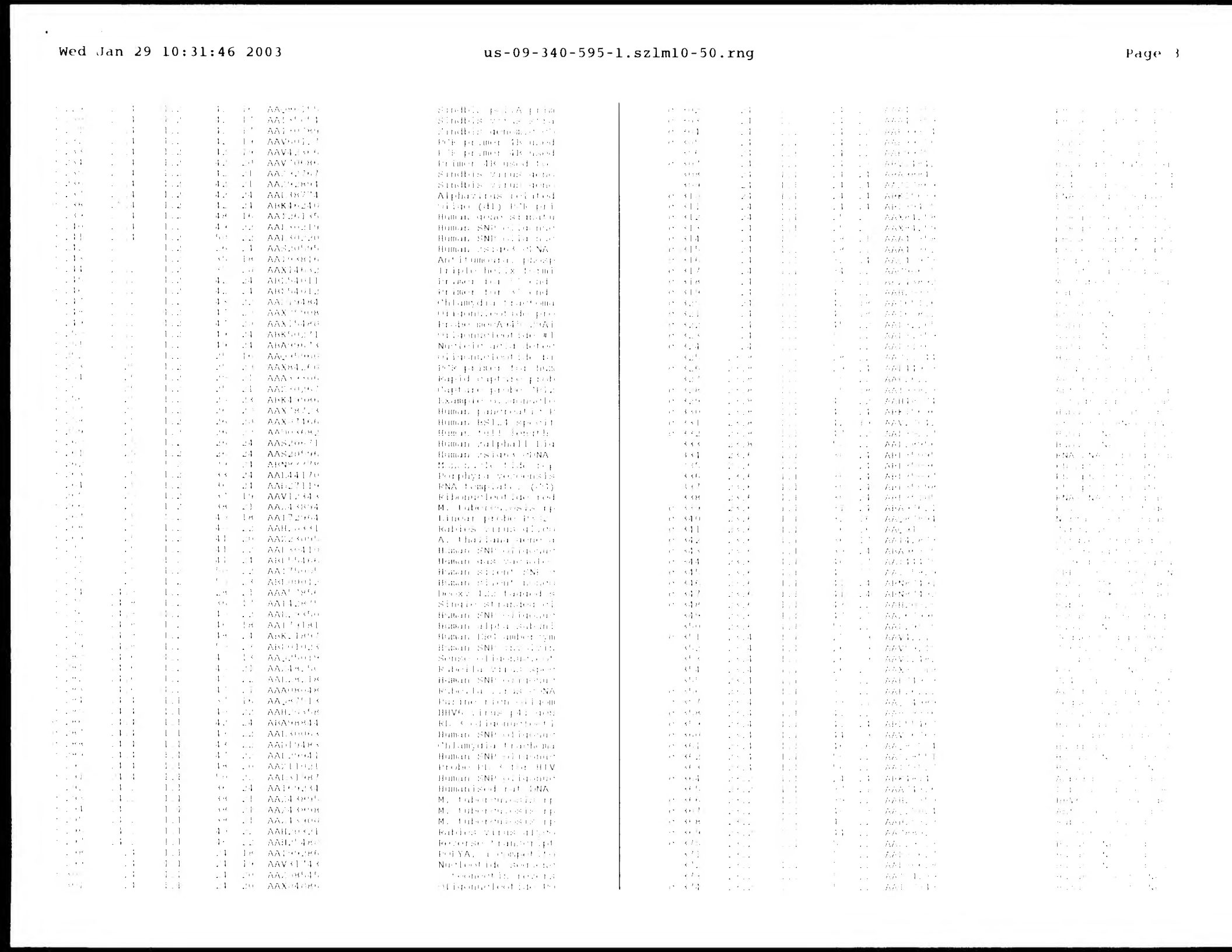

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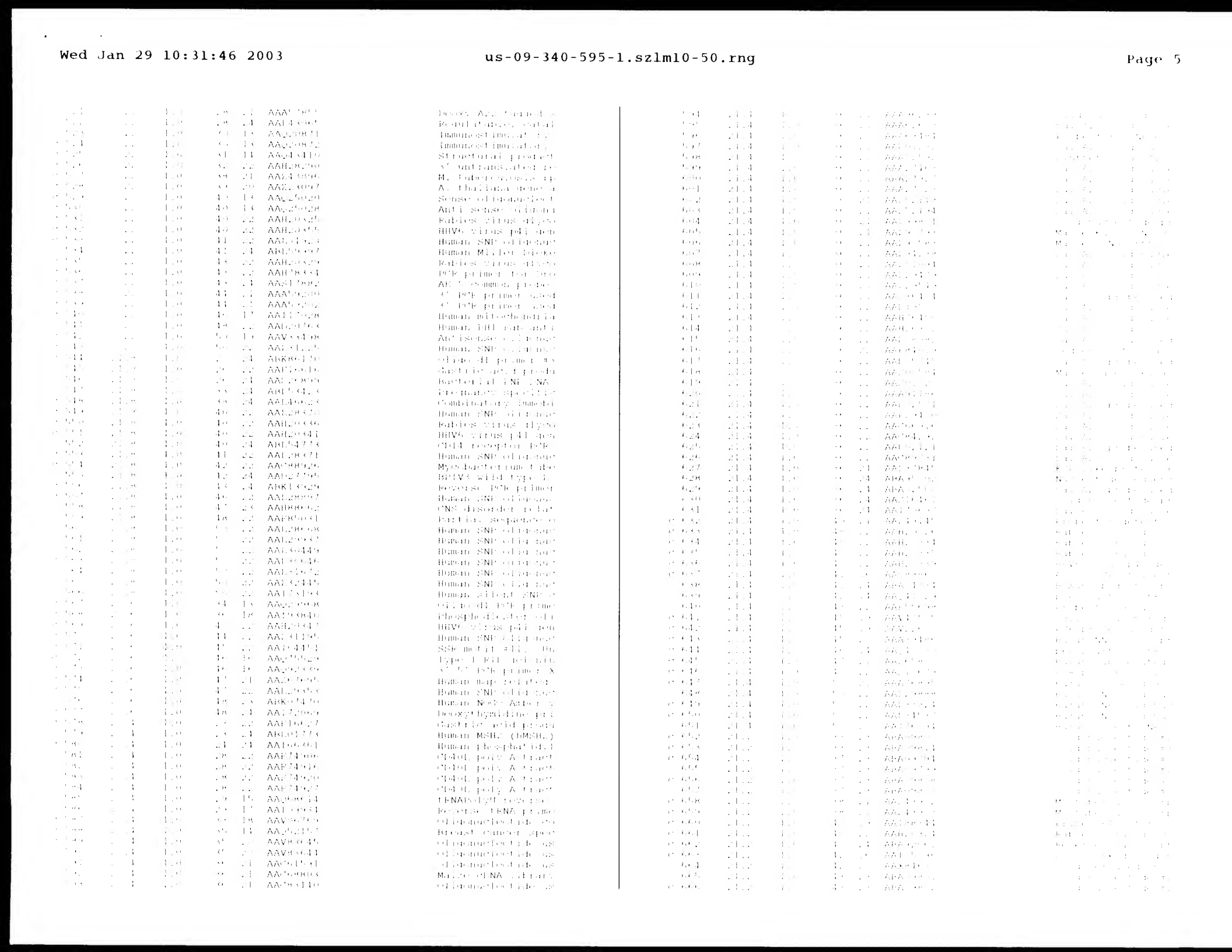
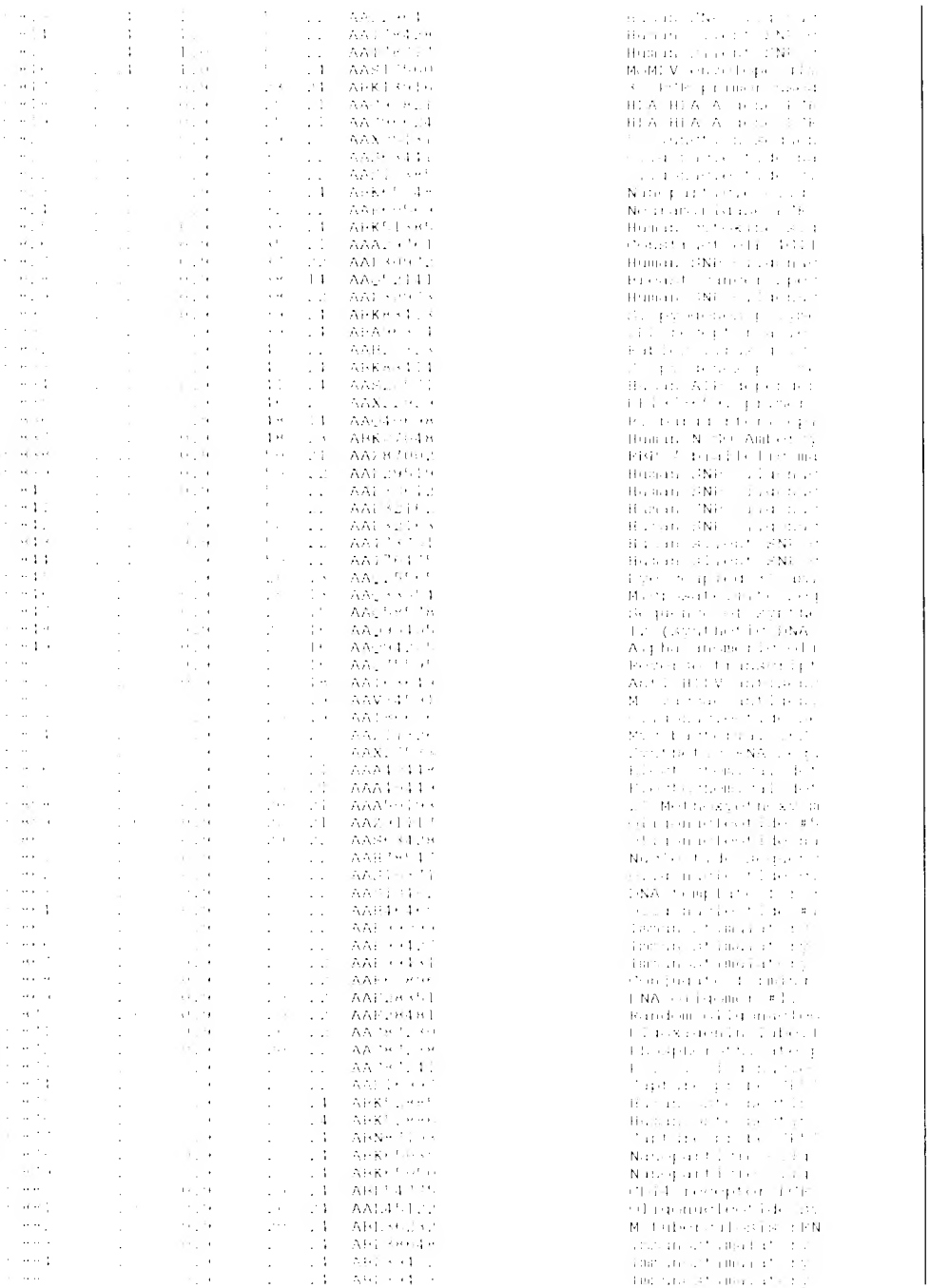
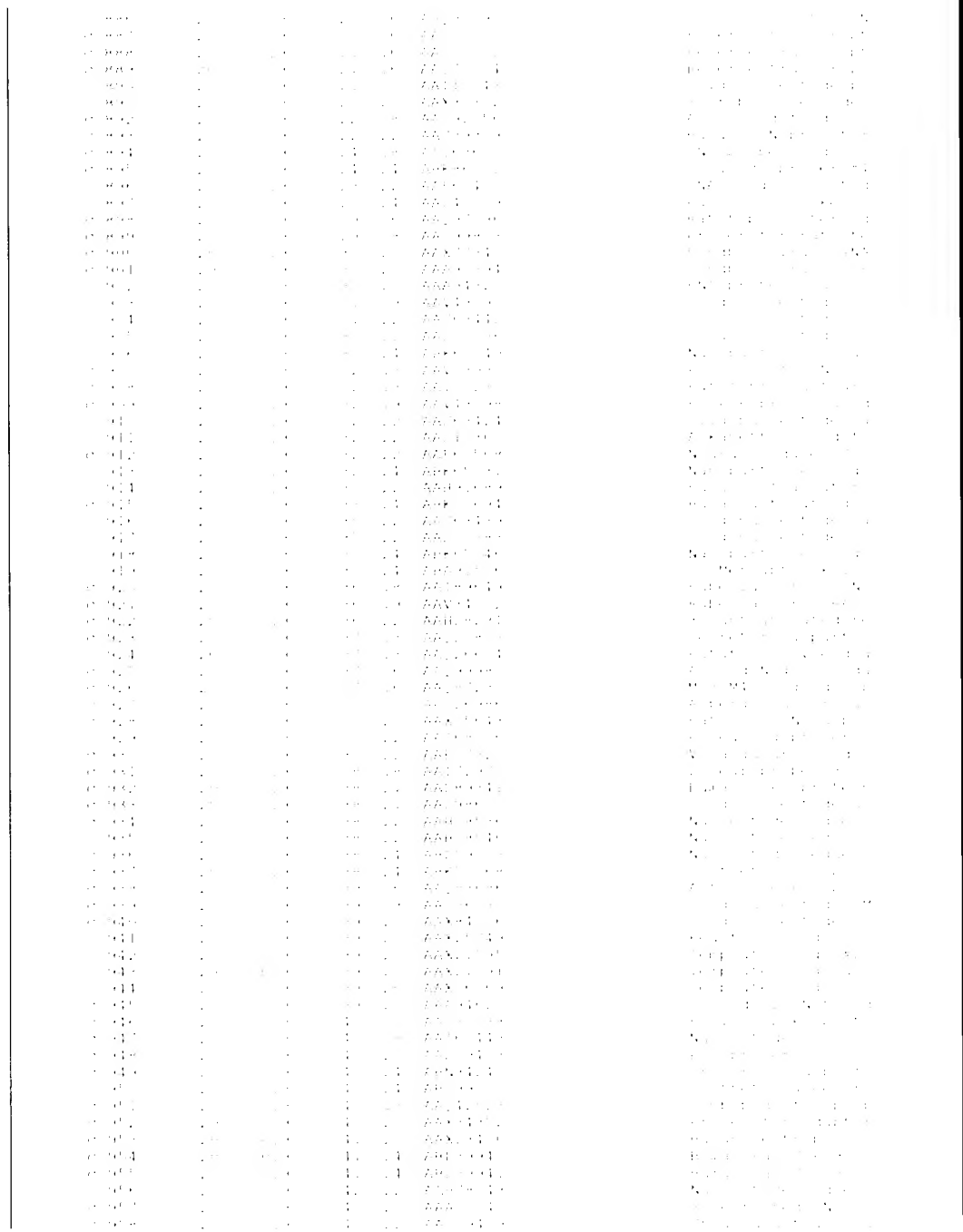






c 95	21	0.9	43	22	AAD19486	Chlamydia t rachoma
96	20	0.9	45	16	AAI26202	Human gene signat
c 96	20	0.9	45	22	AAI29557	Human SNP oligonuc
c 96	20	0.9	45	22	AAI68557	Linker primer. Hu
c 96	20	0.9	45	22	AAS22425	Human collagen alp
96	20	0.9	48	22	AAI71163	Human silen DNI
c 96	20	0.9	49	19	AAV23404	Poliovirus DNA pri
96	20	0.9	49	21	ABN75029	Human MAGPIX at cM
c 96	20	0.9	50	22	AAL31221	Human SNP oligonuc
96	20	0.9	50	22	AAL32227	Human SNP oligonuc
c 96	20	0.9	50	22	AAI72529	Human silen SNP o
97	20	0.9	50	22	AAI78141	Human silen SNP o
97	20	0.9	50	23	ABL00015	Human silen nonco
c 97	19.8	0.9	24	22	AAH44623	Human PD 17 PCR pr
97	19.8	0.9	24	24	ABK12409	RT PCR primer #1 t
97	19.8	0.9	27	22	AAH14980	Nucleotide sequenc
c 97	19.8	0.9	28	14	AAQ36362	GL6anti, targetted
97	19.8	0.9	28	22	AAF74909	CD40L poly-A tract
97	19.8	0.9	28	22	AAF74910	CD40L poly-A tract
97	19.8	0.9	28	22	AAF74914	CD40L poly-A tract
c 97	19.8	0.9	29	19	AAV61142	Mouse CD2K exon 1
98	19.8	0.9	32	20	AAX61751	Allelic ladder fo
c 98	19.8	0.9	33	14	AAQ24747	V gamma 1.4 sequen
c 98	19.8	0.9	33	22	AAH28289	3' untranslated re
c 98	19.8	0.9	34	22	AAS06970	Reverse PCR primer
c 98	19.8	0.9	35	18	AAI93899	Phosphatidylser eli
c 98	19.9	0.9	37	17	AAI72869	Control triplex to
c 98	19.9	0.9	39	19	AAV17511	Primer CHK2 1a c
c 98	19.8	0.9	40	14	AAQ36399	BPV-1 L1 gene prim
c 98	19.8	0.9	42	23	ABL00294	Human silen nonco
c 98	19.8	0.9	44	16	AAI51102	Fragment of cDNA c
c 99	19.8	0.9	44	19	AAV30856	Human WBP1 hybridi
99	19.8	0.9	45	21	AAC55122	Arabidopsis thalia
99	19.8	0.9	47	20	AAX30238	PCR amplification
c 99	19.8	0.9	47	21	AAZ65918	Human map-related
c 99	19.8	0.9	47	21	AAZ66174	Human map-related
99	19.8	0.9	47	21	AAZ68125	Human map-related
99	19.8	0.9	48	24	ABK21417	Human ERG amber sym
c 99	19.8	0.9	49	24	ABK52264	EJB016 DNA linker
99	19.8	0.9	49	24	ABN75342	Human SYCP1 cDNA
c 99	19.8	0.9	50	16	AAQ24745	VEGF 2' NDL DNA se
c10	19.8	0.9	50	19	AAV36666	Circular oligonucl

ALIGNMENTS

RESULT 1
AAS95728/c
ID AAS95728 standard; DNA; 45 BP.
XX
AC AAS95728;
XX
DT 14-FEB-2002 (first entry)
XX
DE Allele discrimination PI primer #12.
XX
KW Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; fragile X syndrome;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.
XX
OS Homo sapiens.
XX
PN WO200177766-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US11151.
XX

PR 05-APR-2000; 2000US-0194511.
XX
PA (MOLE-) MOLECULAR STAGING INC.
XX
PI Abarzua P;
XX
DR WPI; 2002-041057/06.
XX
PT Detecting single nucleotide polymorphism involves amplifying target
PT sequences using small primer probe that matches or mismatches to target
PT sequence and extendible primer probe which is then detected
XX
PS Claim 15; Page 41; 67pp; English.
XX
CC The invention relates to detecting single nucleotide polymorphism by
CC contacting an allele specific oligonucleotide primer (PI) with a target
CC polynucleotide to form a hybridisation complex, where the target sequence
CC is complementary to PI at one end but the terminal nucleotide at the
CC third nucleotide from the terminal at the other end of PI may not be
CC complementary. The complex is then treated with a DNA polymerase
CC deficient DNA polymerase enzyme under conditions that promote extension
CC of PI at the 3' end using the target as the template. The polymerase
CC extension of PI. The oligonucleotide primers optionally have a target
CC polynucleotide distinguish between matched and mismatched target. In
CC the absence of sequence amplification indicates the presence of a single
CC nucleotide mismatch. Primer sequences complementary to a sequence that
CC amplification target circle can be used in rolling circle amplification
CC (RCA). The method is useful for diagnosing a disease caused by, related
CC by or related to a mutation in at least one gene, such as Parkinson's
CC disease, polycystic kidney disease, fragile X syndrome, Huntington's
CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC fluorescence decorators used in the detection of RCA products.
XX
SQ Sequence 45 BP; 9 A; 8 C; 13 G; 15 T; 0 other;

Query Match 1.7%; Score 19.8; DB 24; Length 45;
Best Local Similarity 42.9%; Pred. No. 0.0000021;
Matches 18; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2094 tttttttttttttttttttttttttttttttttttttttttt 2138
||||||||||||||||||||||||||||||||||||||||||||
DB 45 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1

RESULT 2
AAS95724/c
ID AAS95724 standard; DNA; 45 BP.
XX
AC AAS95724;
XX
DT 14-FEB-2002 (first entry)
XX
DE Allele discrimination PI primer #9.
XX
KW Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; fragile X syndrome;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.
XX
OS Homo sapiens.
XX
PN WO200177766-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US11151.
XX

PT Detecting single nucleotide polymorphism involves amplifying target
PT sequences using small primer probe that matches or mismatches to target
PT sequence and extending primer probe which is then detected.
XX
PS Claim 15; Page 42; 67pp; English.
XX
CC The invention relates to detecting single nucleotide polymorphisms by
CC contacting an allele-specific oligonucleotide primer (Pl) with a target
CC polynucleotide to form a hybridisation complex, where the target sequence
CC is complementary to Pl at one end but the terminal nucleotide and the
CC third nucleotide from the terminal at the other end of Pl may not be
CC complementary. The complex is then contacted with an exonuclease
CC deficient DNA polymerase enzyme under conditions that promote extension
CC of Pl with the target DNA as the template, thereby forming an extended
CC segment of Pl. Oligonucleotide probes hybridising to one or more target
CC polynucleotides distinguish between matched and mismatched 3' ends. Hence
CC the absence of sequence amplification indicates the presence of a single
CC nucleotide mismatch. Primer sequences complementary to a sequence on an
CC amplification target circle can be used in rolling circle amplification
CC (RCA). The method is useful for diagnosing a disease caused by, induced
CC by or related to a mutation in at least one gene, such as Parkinson's
CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC melanoma. Sequences AAS95711 AAS95745 represent primers, targets and
CC fluorescence decorators used in the detection of RCA products.
XX
SQ Sequence 46 BP; 8 A; 4 C; 0 G; 39 T; 0 other;

Query Match 1.6%; Score 44.2; DB 24; Length 46;
Best Local Similarity 92.3%; Pred. No. 4.9e-02;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2095 TATAAATTATAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
|||||||||||||||||||||||||||||||||||||||
Db 40 TATAAATTATAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA 1

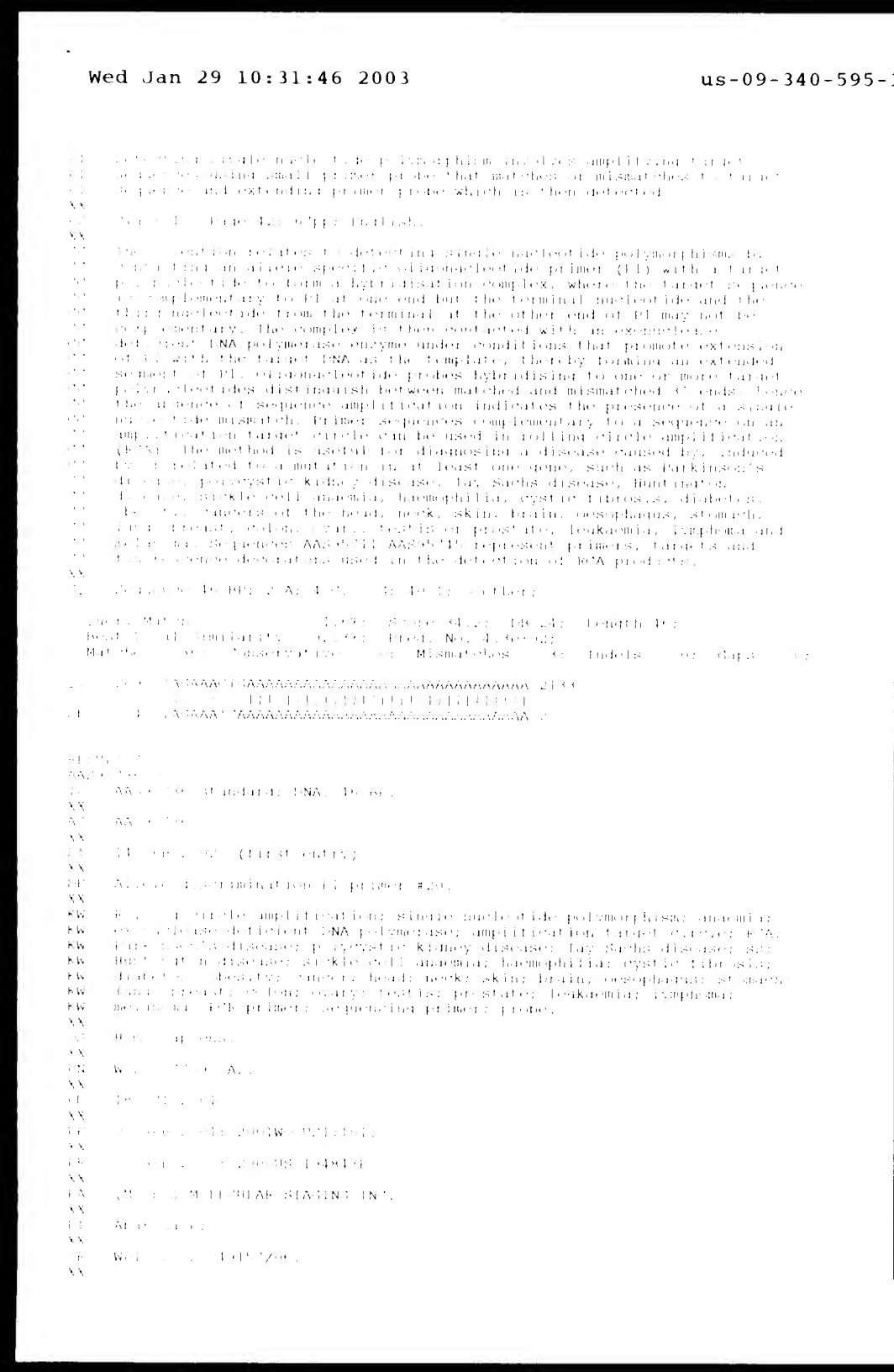
RESULT 5
AAS95742/c
ID AAS95742 standard; DNA; 46 BP.
XX
AC AAS95742;
XX
DT 14-FEB-2002 (first entry)
XX
DE Allele discrimination Pl primer #16.
XX
KW Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.
XX
OS Homo sapiens.
XX
PN WO200177390-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011511.
XX
PR 05-APR-2000; 2000US-194834P.
XX
PA (MOLE-) MOLECULAR STAGING INC.
XX
PI Abarzua P;
XX
DR WPI; 2002-049197/06.
XX

PT Detecting single nucleotide polymorphism involves amplifying target
PT sequences using small primer probe that matches or mismatches to target
PT sequence and extending primer probe which is then detected.
XX
PS Claim 15; Page 42; 67pp; English.
XX
CC The invention relates to detecting single nucleotide polymorphisms by
CC contacting an allele-specific oligonucleotide primer (Pl) with a target
CC polynucleotide to form a hybridisation complex, where the target sequence
CC is complementary to Pl at one end but the terminal nucleotide and the
CC third nucleotide from the terminal at the other end of Pl may not be
CC complementary. The complex is then contacted with an exonuclease
CC deficient DNA polymerase enzyme under conditions that promote extension
CC of Pl with the target DNA as the template, thereby forming an extended
CC segment of Pl. Oligonucleotide probes hybridising to one or more target
CC polynucleotides distinguish between matched and mismatched 3' ends. Hence
CC the absence of sequence amplification indicates the presence of a single
CC nucleotide mismatch. Primer sequences complementary to a sequence on an
CC amplification target circle can be used in rolling circle amplification
CC (RCA). The method is useful for diagnosing a disease caused by, induced
CC by or related to a mutation in at least one gene, such as Parkinson's
CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC melanoma. Sequences AAS95711 AAS95745 represent primers, targets and
CC fluorescence decorators used in the detection of RCA products.
XX
SQ Sequence 46 BP; 8 A; 4 C; 0 G; 39 T; 0 other;

Query Match 1.6%; Score 44.2; DB 24; Length 46;
Best Local Similarity 92.3%; Pred. No. 4.9e-02;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2095 TATAAATTATAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
|||||||||||||||||||||||||||||||||||||||
Db 40 TATAAATTATAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 6
AAS95745/c
ID AAS95745 standard; DNA; 46 BP.
XX
AC AAS95745;
XX
DT 14-FEB-2002 (first entry)
XX
DE Allele discrimination Pl primer #19.
XX
KW Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.
XX
OS Homo sapiens.
XX
PN WO200177390-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011511.
XX
PR 05-APR-2000; 2000US-194834P.
XX
PA (MOLE-) MOLECULAR STAGING INC.
XX
PI Abarzua P;
XX
DR WPI; 2002-049197/06.
XX



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DT   03-JUN-2000.
XX
DT    2-DEC-1999;   99WO-US28472.
XX
DT   12-DEC-1998;   98US-0111945.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Lohse P,  Kurz M,  Wagner R;
XX
DR   WPI; 2000-412459/35.
XX
PT   Generating a DNA-protein fusion useful for selecting a desired protein
PT   or the encoding DNA, comprises covalently linking proteins with their
PT   encoding DNA sequences.
XX
PS   Disclosure; Page 16; 51pp; English.
XX
CC   The present invention relates to methods of covalently tagging proteins
CC   with their encoding DNA sequences. Several methods may be used to create
CC   these DNA-protein fusions. In general, the methods involve linking a
CC   primer to an RNA molecule, then translating the RNA to produce a protein
CC   which is bound to the primer. The RNA is then reverse transcribed to
CC   give a DNA-protein fusion. The present sequence is model linker #6
CC   that was used to demonstrate DNA protein fusion formation. This
CC   sequence bound mRNA #2 (see AAA61755). The psoralen modification allowed
CC   the linker to bind the mRNA, the puromycin-CPG modification allowed
CC   the linker to bind the protein. The DNA-protein fusions are useful in
CC   binding and molecular recognition assays that involve biological
CC   materials containing ribonucleases. The covalent bond between the
CC   protein and the encoding DNA makes the fusion more stable than
CC   RNA protein fusions. This means selection experiments could be
CC   limited to extremely mild reaction conditions.
XX
SQ   Sequence 47 BP; 33 A; 4 C; 7 G; 3 T; 0 other;

  Query Match             1.6%;  Score 33.8;  DB 21;  Length 47;
  Best Local Similarity   94.6%;  Pred. No. 5.8e-02;
  Matches   35;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47
          |||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47


RESULT 9
AAF60446
ID   AAF60446 standard; DNA; 47 BP.
XX
AC   AAF60446;
XX
DT   27-APR-2001  (first entry)
XX
DE   DNA oligonucleotide #4.
XX
KW   Protein-RNA fusion; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1%
FT                    /*tag= a
FT                    /mod_base= OTHER
FT                    /note= "5' A, where X is a Psoralen linker"
FT   modified_base    47
FT                    /*tag= b
FT                    /mod_base= OTHER
FT                    /note= "3' Pu, where Pu is puromycin-CPG"
XX
PN   WO200176552-A1.
XX
PD   11-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US11945.
XX
PR   12-APR-2000; 2000US-0548121.
XX
PA   (GENE-) GENETICS INST LLC.
XX
PI   Bee G,  Kobie JJ,  Kurt I,  Lohse J,  Vrocalis D;
XX
DR   WPI; 2001-649245/73.
XX
PT   Determining the presence of a YB1/p50 target sequence in a DNA sample
PT   containing YB1/p50 protein, useful for detecting genetic
PT   polymorphisms, comprises determining the amount of labelled probe
PT   bound to the target sequence
XX
PS   Example 2; Figure 6; 99pp; English.
XX
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```
PF   19-JUL-2000; 2000WO-US19807.
XX
PR   27-JUL-1999;  99US-0145881P.
XX
PA   (GNEL ) GNEL S INC.
XX
PI   Kurz M,  Lohse P,  Wagner R;
XX
DR   WPI; 2001-163883/18.
XX
PT   Affixing a peptide acceptor to an RNA molecule useful in in vitro
PT   fusion proteins for isolating proteins or nucleic acids with desired
PT   properties through attachment of a peptide acceptor to the 3' end of
PT   RNA molecule
XX
PS   Example 5; Page 27; 51pp; English.
XX
CC   The present invention relates to a method for affixing a peptide acceptor
CC   to an RNA molecule through the formation of a covalent bond, or by
CC   bond, or by chemical ligation. The method is useful for producing
CC   RNA-protein fusions which can be used for the isolation of proteins
CC   nucleic acids with desired properties from large pools of partially
CC   completely random amino acid or nucleic acid sequences. The present
CC   sequence is a DNA oligonucleotide used in the present invention.
XX
SQ   Sequence 47 BP; 33 A; 3 C; 7 G; 3 T; 0 other;

  Query Match             1.6%;  Score 33.8;  DB 22;  Length 47;
  Best Local Similarity   94.6%;  Pred. No. 5.8e-02;
  Matches   35;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47
          |||||||||||||||||||||||||||||||||||||||||||
Db      1 GGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47


RESULT 10
ABK80210
ID   ABK80210 standard; DNA; 47 BP.
XX
AC   ABK80210;
XX
DT   27-APR-2001  (first entry)
XX
DE   CYP2D6 gene polymorphism detection primer #10.
XX
KW   Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200166810-A1.
XX
PD   20-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US18901.
XX
PR   12-JUN-2000; 2000US-0592111.
XX
PA   (GENE-) GENOMIC HEALTH INC.
XX
PI   Bee G,  Kobie JJ,  Kurt I,  Lohse J,  Vrocalis D;
XX
DR   WPI; 2002-140245/17.
XX
PT   Determining the presence of a YB1/p50 target sequence in a DNA sample
PT   containing YB1/p50 protein, useful for detecting genetic
PT   polymorphisms, comprises determining the amount of labelled probe
PT   bound to the target sequence
XX
PS   Example 2; Figure 6; 99pp; English.
XX
```

CC the position at which (B') is to be bonded, preparing (B') and reacting
CC (A') and (B'); and (ii) the use of aryl groups (II) (optionally bonded
CC via a chemical group) for transporting (A) across biological membranes.
CC The products of the invention have cytostatic, virucide, vasotropic,
CC dermatological, antipsoriatic and antiasthmatic activity and can be used
CC for gene therapy. Conjugation of (A) with (B) is useful for transporting
CC (A) across biological membranes or into eukaryotic or prokaryotic cells
CC (specifically bacterial, yeast or mammalian cells, including human cells,
CC particularly tumor cells). Medicaments, diagnostic agents and test kits
CC containing (I) are also claimed. Typically, (I) are antisense
CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
CC treating viral infections or diseases associated with interins or
CC cell-cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma);
CC or labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
CC hybridization. Conjugation with (B) markedly improves the cellular uptake
CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
CC in which case the conjugates (I) are thus useful, inter alia, in
CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
CC is superior to that obtained using other receptor mediated
CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
CC the scope of (B)) have superior uptake to corresponding fluorescein
CC conjugates.
XX
SQ Sequence 50 BP; 50 A; 0 C; 0 G; 0 T; 0 other;

Query Match 1.5%; Score 32.4; DB 22; Length 50;
Best Local Similarity 78.0%; Pred. No. 1.1e-04;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50
|||| || | | ||| ||||||||||||||||||||||||||||||||||||||||||
Db 1 GGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50

RESULT 13
AAS58336/c
ID AAS58336 standard; cDNA; 50 BP.
XX
AC AAS58336;
XX
DT 13-FEB-2002 (first entry)
XX
DE cDNA #1012 encoding portion of a human colon tumour protein.
XX
KW Human; colon tumour protein; colon cancer; gene therapy; cytostatic ss.
XX
OS Homo sapiens.
XX
PN WO200177327-A2.
XX
PD 18-OCT-2001.
XX
PF 12-MAR-2001; 2001WO-US008346.
XX
PR 14-MAR-2000; 2000US-189547P.
PR 04-MAY-2000; 2000US-202024P.
PR 05-MAY-2000; 2000US-202189P.
XX
PA (ZOLT-) ZORTIA CORP.
XX
PI Meagher M.J, Xu J, King GE;
XX
DR WPI; 2001-611627/70.
XX
PT New colon tumour proteins and related nucleic acid, useful for
PT treatment, prevention, diagnosis and monitoring of cancer.
XX
PS Claim 4; Page 216; 299pp; English.
XX
CC The present invention relates to the isolation of novel cDNA sequences
CC encoding for at least an immunogenic portion of human colon tumour
CC proteins. The sequences of the invention are useful in pharmaceutical
CC compositions and vaccines for the prevention and treatment of cancers
CC such as colon cancer. They are also useful for the diagnosis and
CC monitoring of such cancers. Antibodies to the novel tumour proteins
CC and antisera prepared from cells that express these tumour proteins
CC colon tumour proteins can be used to inhibit the growth of
CC cancers, especially those responsive specifically with colon tumour proteins
CC are useful for detecting tumour cells from samples (e.g. biopsies) for
CC for cancer treatment. The polynucleotides sequences are also useful in
CC gene therapy. AAS57342-AAS58005 represent the cDNA sequences of the
CC invention that encode for portions of human colon tumour proteins.
XX
SQ Sequence 50 BP; 7 A; 0 C; 43 G; 0 T; 0 other;

Query Match 1.5%; Score 32.4; DB 24; Length 50;
Best Local Similarity 78.0%; Pred. No. 1.1e-04;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50
|||| || | | ||| ||||||||||||||||||||||||||||||||||||||||||
Db 1 GGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50

RESULT 14
ABN89414/c
ID ABN89414 standard; DNA; 50 BP.
XX
AC ABN89414;
XX
DT 30-AUG-2001 (first entry)
XX
DE Polymorphism detection in mass spectroscopy ss.
XX
KW Polymorphism; mass spectroscopy ss.
XX
OS Synthetic.
XX
PN WO200157257-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003741.
XX
PR 02-FEB-2000; 2000US-179041.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Inoko H, Tamiya G, Nakajima K, Kimura N, Nanashima S, Matsuura M,
PI Okamoto K;
XX
DR WPI; 2002-508814/54.
XX
PT Detection of DNA polymorphism by mass spectroscopy for identification
PT and diagnosis of gene related diseases.
XX
PS Example 5; Page 27; 48pp; Japanese.
XX
CC The present invention describes a method for determining a single
CC DNA bp; (a) preparing a DNA sample to be analysed containing the DNA
CC region in which the target polymorphism is located; (b) hybridising
CC an appropriate oligonucleotide fragment, immobilised on a support, and
CC (c) detecting the hybridised target DNA by mass spectroscopy. The method
CC can be used for the investigation and diagnosis of genetic diseases.
CC The method allows polymorphisms to be detected rapidly and with accuracy
CC in a large number of specimens. The present sequence represents an
CC oligonucleotide which is used in an example from the present invention.
XX
SQ Sequence 50 BP; 7 A; 0 C; 43 G; 0 T; 0 other;

Query Match 1.5%; Score 32.4; DB 24; Length 50;
Best Local Similarity 78.0%; Pred. No. 1.1e-04;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50
|||| || | | ||| ||||||||||||||||||||||||||||||||||||||||||
Db 1 GGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50

```
AC   AAA94419;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 42-P[CHE].
XX
KW   RNA protein fusion; protein library; protein isolation; DNA-RNA hybrid;
KW   gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1..13
FT                   /*tag= a
FT                   /label= RNA
FT   modified_base   42
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-US03259.
XX
PR   12-FEB-1999;  99US-0247190.
XX
PA   (SEBO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW, Roberts RW, Liu R;
XX
DR   WPI; 2000-511922/46.
XX
PT   In vitro protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA protein fusions and incubating these protein fusions under
PT   high salt conditions -
XX
PS   Disclosure; Page 44; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides used
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form.
XX
SQ   Sequence 42 BP; 31 A, 4 C, 6 G, 1 U, 0 other.

  Query Match             1.5%;  Score 42;  DB 2;  Length 42;
  Best Local Similarity   96.9%;  Pred. No. 1.2e+03;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 AACUGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33
          ||||||||||||||||||||||||||||||||||
Db      9 AACUGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40


RESULT 28
AAV48091
ID   AAV48091 standard; DNA; 1 BP.
XX
AC   AAV48091;
XX
DT   27-JUL-1999  (first entry)
XX
DE   Oligonucleotide 43-P-CME.
XX
KW   In situ translation; RNA protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss; DNA/RNA hybrid.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    43
FT                   /*tag= a
FT                   /note= "puromycin"
XX
PN   WO9811788-A1.
XX
PD   26-MAR-1998.
XX
PF   14-JAN-1998;    98WO-US00657.
XX
PR   06-NOV-1997;    97US-0064165.
PR   21-JAN-1997;    97US-0035455.
XX
PA   (GRHP ) GEN HOSPITAL CORP.
XX
PI   Liu R, Roberts RW, Szostak JW;
XX
DR   WPI; 1998-211 ../*.
XX
PT   Selection of specific protein binding by screening protein RNA fusions
PT   generated in vitro or in situ - used in drug, diagnostic and
PT   and antibodies with altered properties, potentially useful as
PT   catalysts or for therapy or diagnosis
XX
PS   Disclosure; Page 89; 96pp; English.
XX
CC   The present invention relates to AAV1 (SEQ ID NO:1), AAV1cre-V1-mod and AAV1a-cre-V1-mod and
CC   variations were used to generate RNA protein fusions. These were used in
CC   the selection of a specific protein-RNA by in vitro or in situ
CC   translation of candidate RNA sequences to produce RNA protein fusions.
CC   that selective specific RNA protein fusions. The method is used to
CC   select proteins (or DNA encoding them) having altered properties,
CC   for identification of new binding reagents, to identify drugs for cell
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow
CC   many rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation
CC   proteins that bind specifically to almost any component of cell, or in
CC   any reaction.
XX
SQ   Sequence 43 BP; 9 A; 4 C; 5 G; 1 T; 24 other;

  Query Match             1.5%;  Score 42;  DB 2;  Length 43;
  Best Local Similarity   96.9%;  Pred. No. 1.2e+03;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 AACUGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33
          ||||||||||||||||||||||||||||||||||
Db      9 AACUGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40


RESULT 29
AAQ25031
ID   AAQ25031 standard; DNA; 1 BP.
XX
AC   AAQ25031;
XX
DT   13-JUL-1999  (first entry)
```

CC amplification method for detecting specific single stranded target
CC nucleic acids in samples using a plurality of probe sets comprising at
CC least 2 probes. Each probe comprises a target specific region and a
CC non-complementary region comprising a primer binding site. The probes
CC in each set are ligated when hybridised to a target nucleic acid and
CC amplified by a primer set. The method is used for detecting a nucleotide
CC polymorphism, especially a single nucleotide polymorphism; detecting
CC multiple single stranded target nucleic acid species in a sample; the
CC detection of multiple amplicons); determining the absolute or relative
CC abundance of multiple single stranded nucleic acids in a sample; and
CC detection of a break point region in rearranged nucleic acids. By using
CC a femtomolar amount of the probes, a large number of different probe
CC sets can be used to simultaneously detect and quantify a corresponding
CC large number of target sequences with high specificity. The present
CC DNA sequence is used in a labelled fluorescent oligonucleotide which is
CC used for the hybridisation selection reaction of human mRNA samples.
XX
SQ Sequence 44 BP; 0 A; 0 C; 0 G; 44 T; 0 other;

Query Match 1.7%; Score 51.6; DB 22; Length 44;
Best Local Similarity 89.5%; Pred. No. 1.5e-08;
Matches 34; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGTA-AGAAAGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 42
| | | ||||||||||||||||||||||||||||||||||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTA 1

RESULT 23
AAV09273
ID AAV09273 standard; cDNA; 44 BP.
XX
AC AAV09273;
XX
DT 17-JUL-1998 (first entry)
XX
DE Nucleotide sequence of the 3' portion of the BCSIL_Dr protein.
XX
KW BCSIL_Dr protein; human adult brain cDNA library; nutritional activity;
KW cytokine activity; cell proliferation/differentiation activity;
KW homology; ss.
XX
OS Homo sapiens.
XX
PN WO9748800-A2.
XX
PD 24-DEC-1997.
XX
PF 20-JUN-1997; 97WO-US010601.
XX
PR 17-JUN-1996; 96US-0664596.
XX
PA (GENY) GENETICS INST INC.
XX
PI Boxman M, Evans C, Jacobs K, LaVallie ER, McCoy JM;
PI Merberg D, Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1998-063142/06.
XX
PT Poly-nucleotide(s) and proteins obtained from human PBMC, dendritic
PT cell, adult brain, foetal brain and adult testes cDNA libraries
PT used in research, detection and therapy of, e.g. cytokine and cell
PT proliferation or differentiation
XX
PS Claim 1; Page 91; 78pp; English.
XX
CC This nucleotide sequence encodes the 3' portion of the BCSIL_Dr protein
CC which was isolated from a human adult brain cDNA library. The products
CC of the polynucleotides of the invention can be used in research,
CC detection and therapy, as they may have nutritional activity, cytokine
CC and cell proliferation/differentiation activity. A search against the
CC Genbank database demonstrated that this sequence has no homology
CC with known sequences.
XX
SQ Sequence 44 BP; 11 A; [illegible]

Query Match [illegible]; Score [illegible]; DB 22; Length 44;
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 34; Conservative [illegible]; Mismatches 4; Indels [illegible]; Gaps [illegible];

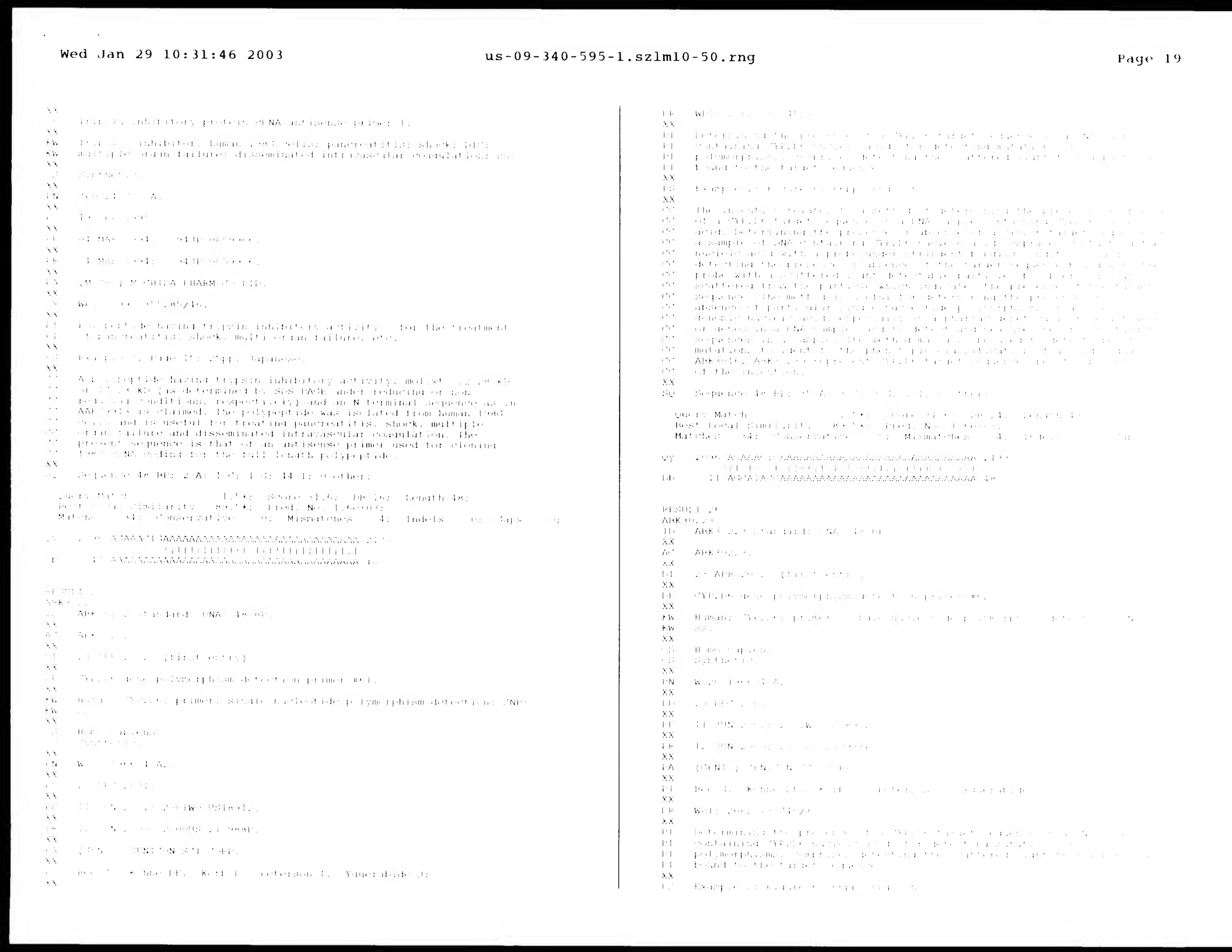
Qy [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTA 42
| | | ||||||||||||||||||||||||||||||||||||
Db [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTA 42

RESULT 24
AAV09273
ID AAV09273 standard; cDNA; 44 BP.
XX
AC AAV09273;
XX
DT 17-JUL-1998 (first entry)
XX
DE Primer for amplifying a target nucleic acid sequence
XX
KW Measurement; cytokine; target nucleic acid; specific primer;
KW hybridisation; amplification; ss.
XX
OS Synthetic.
XX
PN JP2000060587-A.
XX
PD 29-FEB-2000.
XX
PF 21-APR-1999; 99JP-0113967.
XX
PR 21 APR 1998; 98JP-0111847.
XX
PA (GIJU) GIJUTSU KENKYUKI MEAI JEY KYUSHU KIKI.
XX
DR WPI; 2000-241972/21.
XX
PT Measurement of a specific cell activity by using a specific
XX
PS Example 1; Page 9; 14pp; Japanese.
XX
CC The present invention describes a method for measuring (M1) a target
CC nucleic acid (I). The method comprises: (a) combining a sample
CC (I) is combined to a solid phase; (b) hybridising at least one specific
CC primer (II) to (I); (c) extending the 3' terminal of (II) to form
CC presence of a labelled nucleotide; (d) hybridising the extended
CC terminal with an amplification primer; and (e) measuring the label
CC combined to the solid phase. The method is used for the measurement
CC of nucleic acid contained in a trace amount in a sample with high
CC sensitivity. The present sequence represents an oligonucleotide primer
CC for amplifying a nucleic acid by making branches, which is used in the
CC example from the present invention.
XX
SQ Sequence 47 BP; 8 A; 1 C; 1 G; [illegible]

Query Match [illegible]; Score [illegible]; DB 22; Length [illegible];
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches 34; Conservative [illegible]; Mismatches 1; Indels [illegible]; Gaps [illegible];

Qy [illegible] AAAAA-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTA 42
| | | | [illegible]
Db [illegible] A AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTA 46

RESULT 25
AAI04081/c
ID AAI04081 standard; DNA; 18 BP.
XX
AC AAI04081;
XX
DT 16-MAY-2002 (first entry)



XX
CC The invention relates to a method of determining the presence or absence
CC of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC acid. Determining the presence or absence of a CYP2D6 target sequence in
CC a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC nucleic acid with a probe under stringent binding conditions, and
CC detecting the presence or absence of the target sequence bound with the
CC probe with a scattered light detectable particle, by observing light
CC scattered from the particle which indicates the presence of the target
CC sequence. The method is useful for determining the presence or
CC absence of particular single nucleotide polymorphisms or alleles in
CC genomic nucleic acid, especially in a pharmacogenetically relevant gene
CC or genes in a DNA sample, and to detect and measure one or more target
CC sequences in a sample. The method may also be used to detect specific
CC mutations to identify the phenotypic classification of an individual.
CC ABK92162 ABK92240 represent CYP2D6 target sequence-specific primers
CC of the invention.
XX
SQ Sequence 48 BP; [illegible] A; [illegible]

Query Match 1.5%; Score 31.6; DB 24; Length 48;
Best Local Similarity 89.5%; Pred. No. 1.6e-05;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

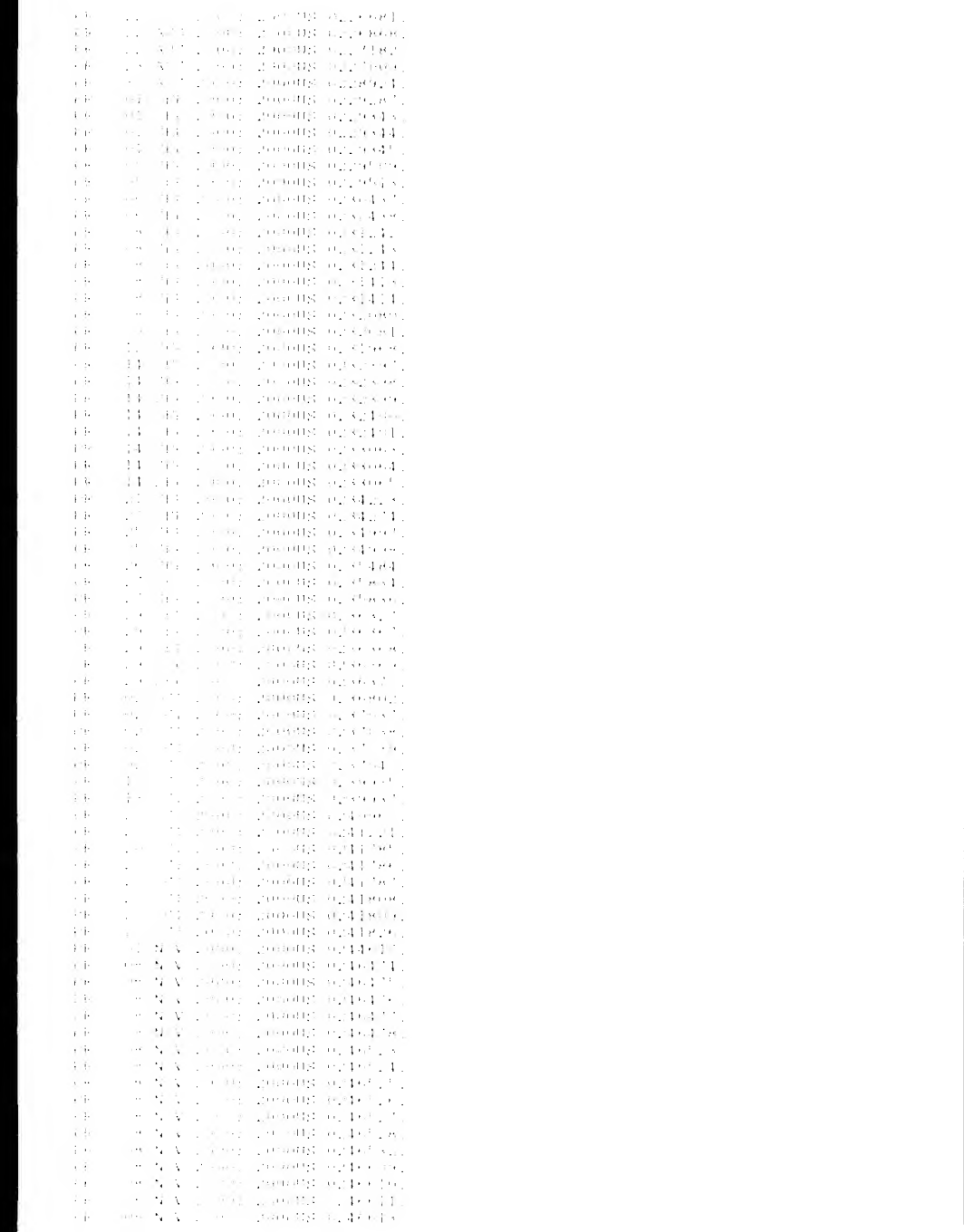
Qy 2096 AAAAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2139
||| | |||||||||||.|||||||||||||||||||||
Db 11 AGTTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 48

RESULT 22
ABK92224
ID ABK92224 standard; DNA; 48 BP.
XX
AC ABK92224;
XX
DT 29-APR-2002 (first entry)
XX
DE CYP2D6 gene polymorphism detection primer #63.
XX
KW Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200190424-A2.
XX
PD 29-NOV-2001.
XX
PF 11-JUN-2001; 2001WO-US019012.
XX
PR 12-JUN-2000; 2000US-210969P.
XX
PA (GENI-) GENICON SCI CORP.
XX
PI Boo G, Kohne DE, Korb L, Peterson T, Yamorabide J;
XX
DR WPI; 2002-130745/17.
XX
PT Determining the presence of a CYP2D6 target sequence in a DNA sample
PT containing CYP2D6 nucleic acid, for detecting mutations or
PT polymorphisms, comprises detecting the scattered light from a particle
PT bound to the target sequence -
XX
PS Example 2; Figure 6; 66pp; English.
XX
CC The invention relates to a method of determining the presence or absence
CC of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC acid. Determining the presence or absence of a CYP2D6 target sequence in
CC a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC nucleic acid with a probe under stringent binding conditions, and
CC detecting the presence or absence of the target sequence bound with the
CC probe with a scattered light detectable particle, by observing light
CC scattered from the particle which indicates the presence of the target
CC sequence. The method is useful for determining the presence or
CC absence of particular single nucleotide polymorphisms or alleles in
CC genomic nucleic acid, especially in a pharmacogenetically relevant gene
CC or genes in a DNA sample, and to detect and measure one or more target
CC sequences in a sample. The method may also be used to detect specific
CC mutations to identify the phenotypic classification of an individual.
CC ABK92162 ABK92240 represent CYP2D6 target sequence-specific primers
CC of the invention.
XX
SQ Sequence 48 BP; [illegible] A; [illegible]

Query Match 1.5%; Score 31.6; DB 24; Length 48;
Best Local Similarity 89.5%; Pred. No. 1.6e-05;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2096 AAAAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2139
||| | |||||||||||.|||||||||||||||||||||
Db 11 AGTTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 48

RESULT 23
AAL07489
ID AAL07489 standard; DNA; 47 BP.
XX
AC AAL07489;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related amplification DNA SEQ ID NO:
XX
KW Human reproductive system related amplification; cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200188205-A2.
XX
PD 22-NOV-2001.
XX
PF 17-JAN-2001; 2001WO-US001555.
XX
PR 31-JAN-2000; 2000US-0179127.
PR 04-FEB-2000; 2000US-0180120.
PR 24-FEB-2000; 2000US-0184981.
PR 02-MAR-2000; 2000US-0186504.
PR 16-MAR-2000; 2000US-0189824.
PR 17-MAR-2000; 2000US-0190356.
PR 18-APR-2000; 2000US-0198126.
PR 19-MAY-2000; 2000US-0205716.
PR 07-JUN-2000; 2000US-0209417.
PR 28-JUN-2000; 2000US-0214800.
PR 30-JUN-2000; 2000US-0215548.
PR 07-JUL-2000; 2000US-0216661.
PR 07-JUL-2000; 2000US-0216844.
PR 11-JUL-2000; 2000US-0217187.
PR 11-JUL-2000; 2000US-0217406.
PR 14-JUL-2000; 2000US-0218271.
PR 26-JUL-2000; 2000US-0221004.
PR 26-JUL-2000; 2000US-0221043.
PR 14-AUG-2000; 2000US-0224713.
PR 14-AUG-2000; 2000US-0224841.
PR 14-AUG-2000; 2000US-0225211.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225302.
PR 14-AUG-2000; 2000US-0225434.
PR 14-AUG-2000; 2000US-0225435.
PR 14-AUG-2000; 2000US-0225436.
PR 14-AUG-2000; 2000US-0225437.
PR 14-AUG-2000; 2000US-0225438.
PR 14-AUG-2000; 2000US-0225439.
PR 14-AUG-2000; 2000US-0225440.
PR 14-AUG-2000; 2000US-0225441.
PR 14-AUG-2000; 2000US-0225442.
PR 14-AUG-2000; 2000US-0225443.
PR 14-AUG-2000; 2000US-0225444.
PR 14-AUG-2000; 2000US-0225445.
PR 14-AUG-2000; 2000US-0225446.
PR 14-AUG-2000; 2000US-0225447.



XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2001096604-A2.
XX
PD 20-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US18912.
XX
PR 12-JUN-2000; 2000US-210988P.
XX
PA (ISLN-) GENICON SCI CORP.
XX
PI Bee G, Kohne DE, Korb L, Peterson I, Ynoverabide J;
XX
DR WPI; 2002-130745/17
XX
PT Determining the presence of a CYP2D6 target sequence in a DNA sample
PT containing CYP2D6 nucleic acid, for detecting mutations or
PT polymorphisms, comprises detecting the scattered light from a parti-le
PT bound to the target sequence
XX
PS Example 2; Figure 6; 66pp; English.
XX
CC The invention relates to a method of determining the presence or absence
CC of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC acid. Determining the presence or absence of a CYP2D6 target sequence in
CC a sample of DNA containing CYP2D6 nucleic acid comprises contacting the
CC nucleic acid with a probe under stringent binding conditions, and
CC detecting the presence or absence of the target sequence bound with a
CC probe with a scattered light detectable particle, by observing light
CC scattered from the particle which indicates the presence of the target
CC sequence. The method is useful for determining the presence or
CC absence of particular single nucleotide polymorphisms or alleles in
CC genomic nucleic acid, especially in a pharmacogenetically relevant gene
CC or genes in a DNA sample, and to detect and measure one or more target
CC sequences in a sample. The method may also be used to detect specific
CC mutations to identify the phenotypic classification of an individual.
CC ABK30215-ABK30230 represent CYP2D6 target sequence specific primers
CC of the invention.
XX
SQ Sequence 49 BP; 33 A; 8 C; 3 G; 5 T; 0 other;

Query Match 1.5%; Score 31.4; DB 24; Length 49;
Best Local Similarity 97.0%; Pred. No. 1.3e-03;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCTCCTCCCAGAAAAAAAAAAGTGCAAAAAAAAAAAAAAA 21
|||||||||||||||||||||||||||||||||||||||||
Db 17 CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 49

RESULT 30
AAQ25023/c
ID AAQ25023 standard; DNA; 49 BP.
XX
AC AAQ25023;
XX
DT 13-JUL-1992 (first entry)
XX
DE Anti-sense oligonucleotide specific for tRNA_lys anti codon region.
XX
KW HIV; thiolation; reverse transcriptase; primer; inhibition;
KW homooligomer; ss.
XX
OS Synthetic.
XX
PN WO9205127-A.
XX
PD 02-APR-1992.
XX
PF 25-AUG-1991; 91WO-US005919.

XX
PR 31-AUG-1990; 90US-576415.
XX
PA (HYNY) HELSINN BIOMEDICAL INST NEW.
XX
PI Barbas CF, Bo YK, Arakawa K, Schultz PG;
XX
DR WPI; 1992-096567/12.
XX
PT Compds. useful for inhibiting viral reverse transcriptase(s) - are
PT thiolated HIV integrase AIDS and pre-AIDS HIV RNA oligo-nucleotides
XX
PS Disclosure; Page 71; 74pp; English.
XX
CC The oligomer comprises an 8-20 nucleotide sequence corresponding to
CC corresponding to the anti-codon region of the reverse transcriptase (RT)
CC primer tRNA_lys, with a 5' terminal thiolated 22 nor homocyclic unit.
CC The homooligomer may be absent and the terminal oligonucleotide is
CC thiolated (e.g. 5' Mercaptan) as in Claim 24. The oligomer is
CC used to inhibit reverse transcriptase in the treatment of HIV
CC See also AAQ22624-27 and AAQ25022-24.
XX
SQ Sequence 49 BP; 7 A; 3 C; 3 G; 3 T; 0 other;

Query Match 1.5%; Score 31.4; DB 15; Length 49;
Best Local Similarity 97.0%; Pred. No. 1.3e-03;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCTCCTCCCAGAAAAAAAAAAGTGCAAAAAAAAAAAAAAA 21
|||||||||||||||||||||||||||||||||||||||||
Db 17 CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 49

RESULT 31
ABK30229
ID ABK30229 standard; DNA; 49 BP.
XX
AC ABK30229;
XX
DT 23-APR-2002 (first entry)
XX
DE CYP2D6 gene polymorphism detection primer #61.
XX
KW Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200196604-A2.
XX
PD 20-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US018912.
XX
PR 12-JUN-2000; 2000US-210988P.
XX
PA (GENI-) GENICON SCI CORP.
XX
PI Bee G, Kohne DE, Korb L, Peterson I, Ynoverabide J;
XX
DR WPI; 2002-130745/17.
XX
PI Determining the presence of a CYP2D6 target sequence in a DNA sample
PI containing CYP2D6 nucleic acid, for detecting mutations or
PI polymorphisms, comprises detecting the scattered light from a particle
PI bound to the target sequence
XX
PS Example 2; Figure 6; 66pp; English.
XX
CC The invention relates to a method of determining the presence or absence
CC of a CYP2D6 target sequence in a DNA sample containing CYP2D6 nucleic
CC acid. Determining the presence or absence of a CYP2D6 target sequence in

```
CC   separated by gel electrophoresis. The present sequence is RNA template,
CC   AU used to direct RNA synthesis by RNA polymerase protein of HCV,
CC   BVDV and polivirus. This sequence is used in the exemplification of
CC   the invention.
XX
SQ   Sequence 36 BP; 34 A; 0 C; 2 G; 0 U; 0 other;

  Query Match             1.5%;  Score 31;  DB 24;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2103 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           |||||||||||||||||||||||||||||||
Db       2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32


RESULT 34
AAD27117
ID   AAD27117 standard; RNA; 36 BP.
XX
AC   AAD27117;
XX
DT   04-APR-2002  (first entry)
XX
DE   RNA template, AU used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non structural protein 5B, NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;  99US-0309670.
XX
PR   11-MAY-1999;  99US-0309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAWR/) LAWR J Y N.
XX
PT   Zhong W.  Hong Z.  Lau JYN.
XX
DR   WPI; 2002-096597/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer -
XX
PS   Example 1; Fig 1A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template
CC   that has an unstable, small stemloop at the 3' end capable of forming
CC   a copy-back structure, a HCV non structural protein 5B (NS5B), ATP,
CC   GTP, CTP, and UTP nucleoside triphosphates (NTPs), where one of the
CC   NTP is radiolabelled and an assay buffer that supports replication
CC   activity of NS5B. The invention also relates to the identification of
CC   optimal properties of an RNA template for copy back self priming RNA
CC   synthesis of HCV. This activity can be used to screen for anti HCV
CC   replicase compounds or to characterise the biological relevance of
CC   lead compounds. The optimal RNA templates can be used for developing
CC   a system to characterise HCV NS5B polymerase mechanistically and
CC   kinetically and for designing small RNA molecules to co-crystallise
CC   with HCV NS5B polymerase. The assay system of the invention is useful
CC   for detecting HCV replicase activity. The nucleic acid synthesised by
CC   NS5B is detected by evaluating an autoradiograph of reaction products
CC   separated by gel electrophoresis. The present sequence is RNA template,
CC   AU used to direct RNA synthesis by RNA polymerase protein of HCV,
CC   BVDV and polivirus. This sequence is used in the exemplification of
CC   the invention.
XX
SQ   Sequence 36 BP; 34 A; 0 C; 2 G; 0 U; 0 other;

  Query Match             1.5%;  Score 31;  DB 24;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2103 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           |||||||||||||||||||||||||||||||
Db       2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32


RESULT 35
AAD27124
ID   AAD27124 standard; RNA; 37 BP.
XX
AC   AAD27124;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, (AU)9 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;  99US-0309670.
XX
PR   11-MAY-1999;  99US-0309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAWR/) LAWR J Y N.
XX
PT   Zhong W.  Hong Z.  Lau JYN.
XX
DR   WPI; 2002-096597/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer -
XX
PS   Example 1; Fig 1A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template
CC   that has an unstable, small stemloop at the 3' end capable of forming
CC   a copy back structure, a HCV non structural protein 5B (NS5B), ATP,
CC   GTP, CTP, and UTP nucleoside triphosphates (NTPs), where one of the
CC   NTP is radiolabelled and in assay buffer that supports replicase
CC   activity of NS5B. The invention also relates to the identification of
CC   optimal properties of an RNA template for copy back self priming RNA
CC   synthesis of HCV. This activity can be used to screen for anti HCV
CC   replicase compounds or to characterise the biological relevance of
CC   lead compounds. The optimal RNA templates can be used for developing
CC   a system to characterise HCV NS5B polymerase mechanistically and
CC   kinetically and for designing small RNA molecules to co-crystallise
CC   with HCV NS5B polymerase. The assay system of the invention is useful
CC   for detecting HCV replicase activity. The nucleic acid synthesised by
CC   NS5B is detected by evaluating an autoradiograph of reaction products
CC   separated by gel electrophoresis. The present sequence is RNA template,
CC   (AU)9 used to direct RNA synthesis by RNA polymerase protein of HCV,
CC   BVDV and polivirus. This sequence is used in the exemplification of
CC   the invention.
XX
SQ   Sequence 37 BP; 32 A; 0 C; 2 G; 3 U; 0 other;
```

```
AAK30211
ID   AAK30211 standard; DNA; 48 BP.
XX
AC   AAK30211;
XX
DT   23-APR-2002  (first entry)
XX
DE   CYP2D6 gene polymorphism detection primer #50.
XX
KW   Human; CYP2D6; primer; single nucleotide polymorphism detection; SNP;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177360-A2.
XX
PD   18-OCT-2001.
XX
PF   05-APR-2001; 2001WO-US011151.
XX
PR   05-APR-2000; 2000US-194844P.
XX
PA   (MYLE ) MYRIAD GENETICS INC.
XX
PI   Abarzua P;
XX
DR   WPI; 2002-043157/06.
XX
PT   Detecting single nucleotide polymorphism involves amplifying target
PT   sequences using small primer probe that matches at mismatches to target
PT   sequence and extended primer probe which is then detected
XX
PS   Claim 15; Page 41; 67pp; English.
XX
CC   The invention relates to detecting single nucleotide polymorphisms by
CC   contacting an allele-specific oligonucleotide primer (P1) with a target
CC   polynucleotide to form a hybridisation complex, where the target sequence
CC   is complementary to P1 at one end but the terminal nucleotide and the
CC   third nucleotide from the terminal at the other end of P1 may not be
CC   complementary. The complex is then contacted with an exonuclease
CC   deficient DNA polymerase enzyme under conditions that promote extension
CC   of P1 using the target DNA as the template, thereby forming an extended
CC   segment of P1. Oligonucleotide probes hybridising to one of more target
CC   polynucleotides distinguish between matched and mismatched 3' ends. Both
CC   the absence of sequence amplification indicates the presence of a single
CC   nucleotide mismatch. Primer sequences complementary to a sequence of a
CC   amplification target circle can be used in rolling circle amplification
CC   (RCA). The method is useful for diagnosing a disease caused by, favored
CC   by or related to a mutation in at least one gene, such as Parkinson's
CC   disease, polycystic kidney disease, Tay Sachs disease, Huntington's
CC   disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC   obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC   lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma or
CC   melanoma. The present AAK30211-AAK30215 represent primers, targets and
CC   fluorescence decorators used in the detection of RCA products.
XX
SQ   Sequence 48 BP; 32 A; 4 C; 7 G; 5 T; 0 other;

  Query Match             1.5%;  Score 31;  DB 24;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-01;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2183 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2152
           |||||||||||||||||||||||||||||||
Db      18 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 49


RESULT 39
AAS95723/c
ID   AAS95723 standard; DNA; 45 BP.
XX
AC   AAS95723;
XX
DT   11-FEB-2002  (first entry)
XX
DE   Allele discrimination P1 primer #7.
```

```
XX
KW   Rolling circle amplification; single nucleotide polymorphism; SNP;
KW   exonuclease deficient DNA polymerase; amplification target; Parkinson's
KW   Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; Huntington
KW   Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW   diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW   lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW   melanoma; PCR primer; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200177360-A2.
XX
PD   18-OCT-2001.
XX
PF   05-APR-2001; 2001WO-US011151.
XX
PR   05-APR-2000; 2000US-194844P.
XX
PA   (MYLE ) MYRIAD GENETICS INC.
XX
PI   Abarzua P;
XX
DR   WPI; 2002-043157/06.
XX
PT   Detecting single nucleotide polymorphism involves amplifying target
PT   sequences using small primer probe that matches at mismatches to target
PT   sequence and extended primer probe which is then detected
XX
PS   Claim 15; Page 41; 67pp; English.
XX
CC   The invention relates to detecting single nucleotide polymorphisms by
CC   contacting an allele-specific oligonucleotide primer (P1) with a target
CC   polynucleotide to form a hybridisation complex, where the target sequence
CC   is complementary to P1 at one end but the terminal nucleotide and the
CC   third nucleotide from the terminal at the other end of P1 may not be
CC   complementary. The complex is then contacted with an exonuclease
CC   deficient DNA polymerase enzyme under conditions that promote extension
CC   of P1 using the target DNA as the template, thereby forming an extended
CC   segment of P1. Oligonucleotide probes hybridising to one of more target
CC   polynucleotides distinguish between matched and mismatched 3' ends. Both
CC   the absence of sequence amplification indicates the presence of a single
CC   nucleotide mismatch. Primer sequences complementary to a sequence of a
CC   amplification target circle can be used in rolling circle amplification
CC   (RCA). The method is useful for diagnosing a disease caused by, favored
CC   by or related to a mutation in at least one gene, such as Parkinson's
CC   disease, polycystic kidney disease, Tay Sachs disease, Huntington's
CC   disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC   obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC   lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma or
CC   melanoma. The present AAK30211-AAK30215 represent primers, targets and
CC   fluorescence decorators used in the detection of RCA products.
XX
SQ   Sequence 48 BP; 2 A; 7 C; 1 G; 38 T; 0 other;

  Query Match             1.4%;  Score 29;  DB 24;  Length 48;
  Best Local Similarity   96.8%;  Pred. No. 2.1e-01;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    2183 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2152
           | | ||||||||||||||||||||||||||||||
Db      48 GTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 17


RESULT 40
AAS95727/c
ID   AAS95727 standard; DNA; 45 BP.
XX
AC   AAS95727;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Allele discrimination P1 primer #11.
```

XX
KW [illegible] amplification; allele-specific oligonucleotide polymorphism;
KW [illegible] detection; DNA polymerase; application; target; virus; mRNA;
KW [illegible] disease; progressive; kidney disease; HIV; Sickle disease; AIDS;
KW Huntington disease; stroke; cancer; breast; neck; skin; brain; oesophagus; stomach;
KW liver; [illegible]; bowel; cervix; testis; prostate; leukaemia; lymphoma;
KW polymerase; PCR primer; sequencing primer; probe.
XX
OS [illegible].
XX
PN WO9[illegible]A2.
XX
PD 31-MAY-1995.
XX
PF 30-NOV-1994; 94WO-[illegible].
XX
PR 30-NOV-1993; 93GB-[illegible].
XX
PA (SENG-) SENSOR CELL INC.
XX
PI Rosbottom MR, [illegible] W, [illegible] S.
XX
DR WPI; [illegible].
XX
PT Specific detection of single nucleotide polymorphisms - by amplifying target
PT nucleic acid sequences.
XX
PS Claim 11; Page 47; [illegible].
XX
AB This invention describes a novel assay for the detection of
AB target nucleic acid sequences and a simple, A preferred target
AB Mycobacterium tuberculosis complex nucleic acid sequence. The detection
AB visual detection of a change in the size of the amplified product
AB instrumentation. Multiple cycles of a strand nucleic acid
AB mixed with first and second detectable primers under [illegible]
AB conditions to [illegible] amplified product [illegible]
AB allowing for [illegible] at the target nucleic [illegible]
AB breaking molecular substrate or inhibits formation [illegible]
AB complex.
XX
SQ Sequence 4 BP; A [illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible] AAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]
[illegible]
Db [illegible] AAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]

FILTER 1:
AAFILE2*
ID AAFILE2* standard; DNA; [illegible] BP.
XX
AC AAFILE2*;
XX
DT [illegible] (Rel. [illegible], Created)
XX
DE Mycobacterium [illegible] rRNA capture probe.
XX
KW Mycobacterium; [illegible] rRNA; [illegible] RNA; [illegible];
KW Mycobacterium [illegible] [illegible] [illegible] [illegible] [illegible];
XX
OS Mycobacterium [illegible]
XX
FH Key Location/Qualifiers
FT misc_feature [illegible]
FT /*tag= a
FT /product= "[illegible]"
FT misc_feature [illegible]
FT /*tag= b
FT /product= "[illegible]"
FT /note= "[illegible]"
FT misc_feature [illegible]
FT /*tag= c
FT /product= "[illegible]"

```
FT                   /note  "2'-O-methoxy-adenosine"
FT   modified_base   4
FT                   /*tag   d
FT                   /mod_base  =m
FT   modified_base   5
FT                   /*tag   e
FT                   /mod_base  =OHC
FT                   /note  "2'-O-methoxy-thymidine"
FT   modified_base   6
FT                   /*tag   f
FT                   /mod_base  =m
FT   modified_base   7
FT                   /*tag   g
FT                   /mod_base  =OHER
FT                   /note  "2'-O-methoxy-thymidine"
FT   modified_base   8
FT                   /*tag   h
FT                   /mod_base  =m
FT   modified_base   9..11
FT                   /*tag   i
FT                   /mod_base  =m
FT   modified_base   12
FT                   /*tag   j
FT                   /mod_base  =m
FT   modified_base   13
FT                   /*tag   k
FT                   /mod_base  =OHER
FT                   /note  "2'-O-methoxy thymidine"
FT   modified_base   14
FT                   /*tag   l
FT                   /mod_base  =OHER
FT                   /note  "2'-O-methoxy-adenosine"
FT   modified_base   15
FT                   /*tag   m
FT                   /mod_base  =OHER
FT                   /note  "2'-O-methoxy-thymidine"
XX
PN   WO-9921992-A2.
XX
PD   ... JUN-2001.
XX
PF   [illegible] 1998:  98WO-US018346.
XX
PR   17-OCT-1997:  97US-0062846.
XX
PA   (SONY ) SEN PROBE INC.
PA   (INMR ) BIOMERIEUX SA.
XX
PI   Prentiano SI,  Jucker MI,  Delgado FD,  Chevrier P,  Rodriguez M;
XX
DR   WPI; 2001-398170/42.
XX
PT   Detecting Mycobacterium species, involves in vitro amplification of 16S
PT   rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT   specific primers, and detecting the amplified nucleic acid -
XX
PS   Example 6; Page 79; 41pp; English.
XX
CC   The invention relates to a method of detecting Mycobacterium species,
CC   that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC   encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC   comprising a polymerase, and at least two primers, and then detecting
CC   the amplified nucleic acid. The method is relatively simple and useful
CC   for detecting the presence of various Mycobacterium species in a
CC   biological sample, and thus important for diagnosis of infections
CC   resulting from them. The method is especially important for screening
CC   opportunistic infections caused by M. tuberculosis or a Mycobacterium
CC   other than tuberculosis (MOTT). The present sequence is a capture
CC   oligomer that includes a sequence that specifically binds to the
CC   Mycobacterium rRNA target sequence and a 3' poly A tail sequence
CC   complementary to an immobilized sequence for capturing the target rRNA
CC   on a solid support.
XX
```

```
SQ   Sequence 18 BP; 5 A; 2 C; 3 G; 8 T; 0 other;

  Query Match             ...1%;  Score ...;  DB ...;  Length 42;
  Best Local Similarity;  ...%;  Pred. No. ...;
  Matches   ...;  Conservative   ...;  Mismatches   ...;  Indels   ...;  Gaps   ...;

Qy      ...NA 21
          ||| | | | | | | | | | | | | | | | | | |
Db      12 GTAGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 42


RESULT 43
AAV41147
ID   AAV41147 standard; DNA; ... BP.
XX
AC   AAV41147;
XX
DT   12-OCT-1998  (first entry)
XX
DE   Nucleotide sequence of the 5' portion of the BCL7 protein.
XX
KW   clone BCL7; secreted protein; human; B-cell lymph; medullary thyroid
KW   antitumour agent; cytostatic; cell proliferative disorder; cancer;
KW   thrombocytosis; ss; ... marker; tumour; diagnostic;
KW   antibody; ds.
XX
OS   Homo sapiens.
XX
PN   WO9821332-A2.
XX
PD   22-MAY-1998.
XX
PF   14-NOV-1997;  97WO-US020411.
XX
PR   14-NOV-1996;  96US-0030918.
PR   15-NOV-1996;  96US-0031211.
PR   02-JUN-1997;  97US-0048076P.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Ardinger MC,  Jarvis K,  Jurata LW,  Moir DM,  Motoyoshi F;
PI   Rubio IA,  Spaulding V,  Thomas M;
XX
DR   WPI; 1998-297495/26.
XX
PT   New nucleic acid encoding secreted protein from human cells
PT   potentially useful, e.g. as immunomodulators, and tumour cell
PT   promoters of tissue growth, haemostatic and thrombolytic agents
XX
PS   Claim 24; Page 71; 99pp; English.
XX
CC   This is the nucleotide sequence of the 5' of the BCL7 protein. The
CC   method of the invention includes secreted proteins that are
CC   potentially useful as immunomodulators, anti-tumour agents, tissue
CC   growth promoters, haemostatic and thrombolytic agents. It was isolated
CC   from a foetal human kidney cDNA library. They may be used in diagnosis
CC   the screening protocols, as tissue/cell-specific probe markers, in
CC   chromosome identification, to identify possible genetic disorders and
CC   isolate new related DNA, as sources of primers for PCR, to generate
CC   anti-probes, ... DNA ... the ... interaction trap assays to
CC   identify sequences that encode interacting proteins.
XX
SQ   Sequence 49 BP; 11 A; ... C; ... G; ... T; ... other;

  Query Match             ...1%;  Score ...;  DB ...;  Length 42;
  Best Local Similarity;  ...%;  Pred. No. ...;
  Matches   ...;  Conservative   ...;  Mismatches   ...;  Indels   ...;  Gaps   ...;

Qy      ...NA 21
          ||| | | | | | | | | | | | | | | | | | |
Db      ... 47
```

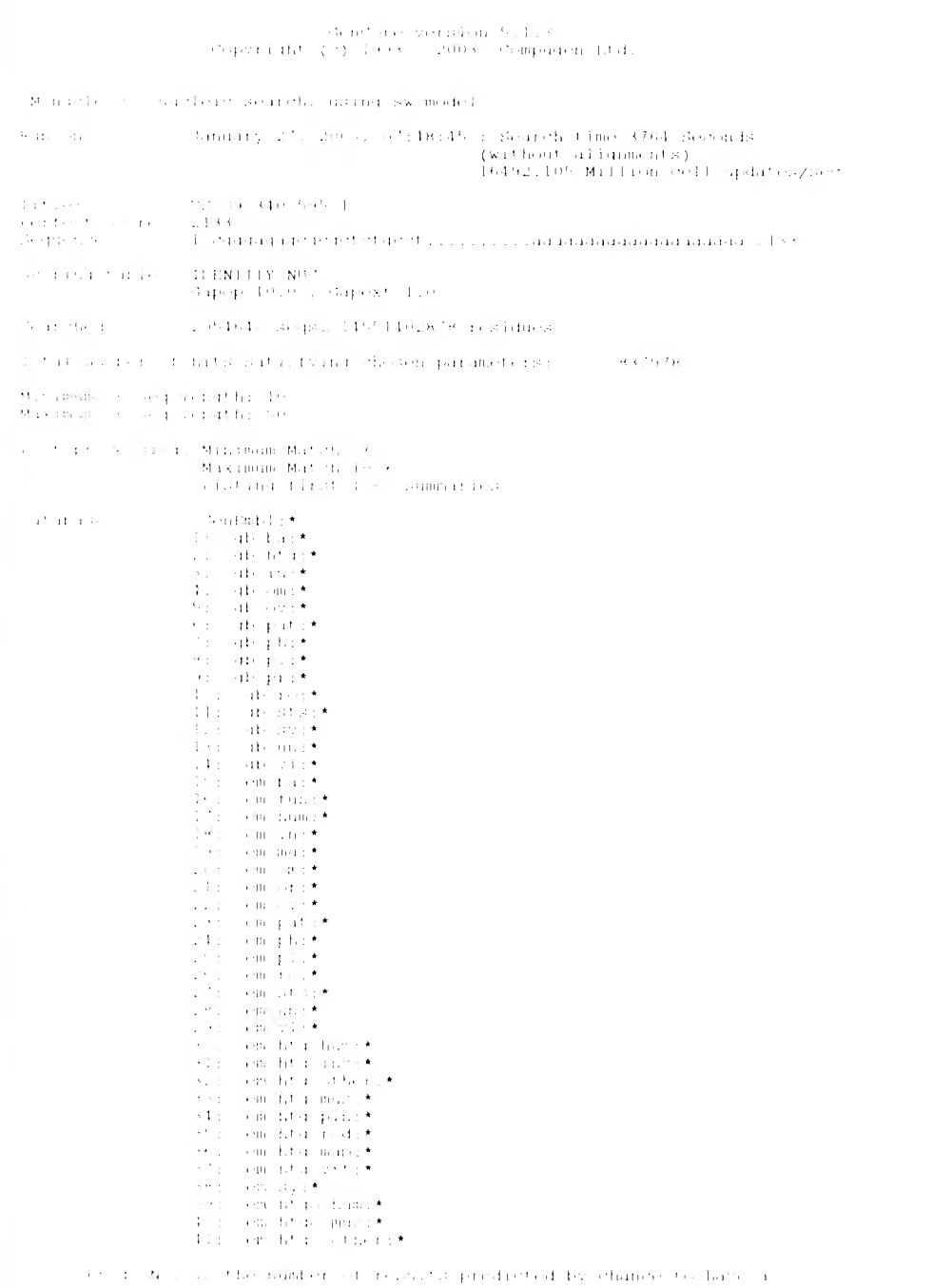
```
DT   17-AUG-2000.
XX
DT   06-FEB-2000; 2000WO-US002789.
XX
PR   09-FEB-1999;   99US-0247190.
XX
PA   (BEBO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW, Roberts RW, Liu R,
XX
DR   WPI; 2000-533022/49.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA protein fusions and incubating these protein fusions under
PT   high salt conditions -
XX
PS   Disclosure; Page 44; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which are
CC   used for the generation of RNA protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA.ribosome.nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readible, nucleic acid form.
XX
SQ   Sequence 42 BP; 32 A; 3 C; 6 G; 1 T; 0 other;

  Query Match             1.4%;  Score 3.1;  DB 21;  Length 42;
  Best Local Similarity   91.8%;  Pred. No. 2.7e+03;
  Matches   30;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    2999 AACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
           ||:||||||||||||||||||||||||||||||||
Db       9 AAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40


RESULT 47
AAV48990
ID   AAV48990 standard; DNA; 43 BP.
XX
AC   AAV48990;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Oligonucleotide 43-P.
XX
KW   In situ translation; RNA protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss; rRNA/cDNA hybrid.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   43
FT                   /*tag= a
FT                   /note  "Puromycin"
XX
PN   WO9841700-A1.
XX
PD   24-SEP-1998.
XX
PF   18-MAR-1998;   98WO-US005403.
XX
PR   06-NOV-1997;   97US-0064114.
PR   21-JAN-1997;   97US-0035403.
XX
PA   (GENE ) GEN HOSPITAL CORP.
XX
PI   Liu R, Roberts RW, Szostak JW;
XX
DR   WPI; 1998-611722/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions
PT   generated in vitro or in situ - useful for, e.g. identifying new DNAs
PT   and antibodies with altered properties, potentially useful as
PT   catalysts or for therapy or diagnosis
XX
PS   Disclosure; Page 39; 94pp; English.
XX
CC   The DNA, RNA and RNA-DNA hybrid sequences of the invention, and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein, or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions, and
CC   then selecting specific RNA protein fusions. The method is used to
CC   select proteins (or DNA encoding them) having altered properties, e.g.
CC   for identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The method involves
CC   many rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation of
CC   proteins that bind specifically to almost any compound or catalyse almost
CC   any reaction.
XX
SQ   Sequence 43 BP; 32 A; 3 C; 6 G; 1 U; 1 other;

  Query Match             1.4%;  Score 3.1;  DB 19;  Length 43;
  Best Local Similarity   91.8%;  Pred. No. 2.8e+03;
  Matches   30;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    2999 AACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2140
           ||:||||||||||||||||||||||||||||||||
Db       9 AAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40


RESULT 48
ABK30219
ID   ABK30219 standard; DNA; 43 BP.
XX
AC   ABK30219;
XX
DT   23-APR-2002  (first entry)
XX
DE   CYP2D6 gene polymorphism detection primer #58.
XX
KW   Human; CYP2D6; primer; allelic nucleotide polymorphism detection; SNP;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200196601-A2.
XX
PD   20-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US018912.
XX
PR   12 JUN 2000; 2000US-0591691.
XX
PA   (GENI-) GENIGEN SCI CORP.
XX
PI   Roe G, Kohne DE, Kolb L, Peterson I, Yguerabide J;
XX
DR   WPI; 2002-136745/17.
```

CC sequence. The method is useful for determining the presence or
CC absence of particular single nucleotide polymorphisms or alleles in
CC genomic nucleic acid, especially in a pharmacogenetically relevant gene
CC or genes in a DNA sample, and to detect and measure one or more target
CC sequences in a sample. The method may also be used to detect specific
CC mutations to identify the phenotypic classification of an individual.
CC [illegible] represents [illegible] target sequence specific primers
CC of the invention.
XX
SQ Sequence 47 BP; 33 A; 3 C; 8 G; 3 T; 0 other;

Query Match 1.4%; Score 30.4; DB 24; Length 47;
Best Local Similarity 96.9%; Pred. No. 2.8e+03;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2102 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
||| ||||||||||||||||||||||||||||||||
Db 14 TGAvTAAAAAAAAAAAAAAAAAAAAAAAAAAA 45

Search completed: January 27, 2003, 08:20:46
Job time : 325 secs



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c	363	21	1.0	46	6	I40484
c	364	21	1.0	46	6	I45570
c	365	21	1.0	50	6	AX161909
	366	20.8	1.0	25	6	AX338548
	367	20.8	1.0	36	6	AX249259
c	368	20.8	1.0	48	6	AX129501
	369	20.8	1.0	48	12	MMHCX21E
	370	20.8	1.0	50	6	AX157157
c	371	20.8	1.0	50	6	AX159192
c	372	20.8	1.0	50	6	AX159191
c	373	20.8	1.0	50	6	AX159496
	374	20.8	1.0	50	6	AX160180
c	375	20.8	1.0	50	6	AX160541
	376	20.8	1.0	50	6	AX111866
	377	20.6	1.0	21	6	AX096834
c	378	20.6	1.0	35	6	AR051295
	379	20.6	1.0	35	6	AX394630
c	380	20.6	1.0	35	6	I16943
c	381	20.6	1.0	35	6	I45737
	382	20.6	1.0	40	6	AR200494
c	383	20.6	1.0	43	6	AX183407
	384	20.6	1.0	45	6	AR022051
	385	20.6	1.0	45	6	AR042918
	386	20.6	1.0	45	6	AR199578
	387	20.6	1.0	45	6	AX096687
c	388	20.6	1.0	47	6	AR200864
c	389	20.6	1.0	47	6	AX156069
c	390	20.6	1.0	48	6	DSP08249
	391	20.6	1.0	50	6	AX159709
	392	20.4	1.0	30	6	AX351710
	393	20.4	1.0	30	6	AX394621
	394	20.4	1.0	31	6	AX394622
	395	20.4	1.0	31	6	AX394623
	396	20.4	1.0	31	6	AX394624
	397	20.4	1.0	32	6	AX394625
	398	20.4	1.0	32	6	AX394626
	399	20.4	1.0	32	6	AX394627
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ALIGNMENTS

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DEFINITION  Human DNA, (library of E.I.A.MacGillivray), and osteosarcoma, cDNA
ACCESSION   M25737 J02863
VERSION     M25737.1  GI:338814
KEYWORDS    osteonectin.
SEGMENT     1 of 10
SOURCE      Human DNA, (library of E.I.A.MacGillivray), and osteosarcoma, cDNA
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            to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Villarreal, L.P., MacGillivray, R.T.A. and Young, E.
  TITLE     Structure, tissue-specific distribution and evolution of [illegible]
            osteonectin sequences
  JOURNAL   Biochemistry 28 (3), [illegible] (1989)
  MEDLINE   89301470
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COMMENT     Draft entry and computer readable sequence for [illegible] by Xia Villarreal.  MAY [illegible]
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ACCESSION   AX287525
VERSION     AX287525.1  GI:17649411
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bruno A.E.
  TITLE     Process [illegible] carbon [illegible] structures
  JOURNAL   Patent: WO [illegible] A [illegible] 20-JUN-2002;
            Molecular Stanford, Inc. (US)
FEATURES             Location/Qualifiers
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BASE COUNT          [illegible]
ORIGIN

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Db       47 [illegible]A 1


RESULT 3
AX287571/c
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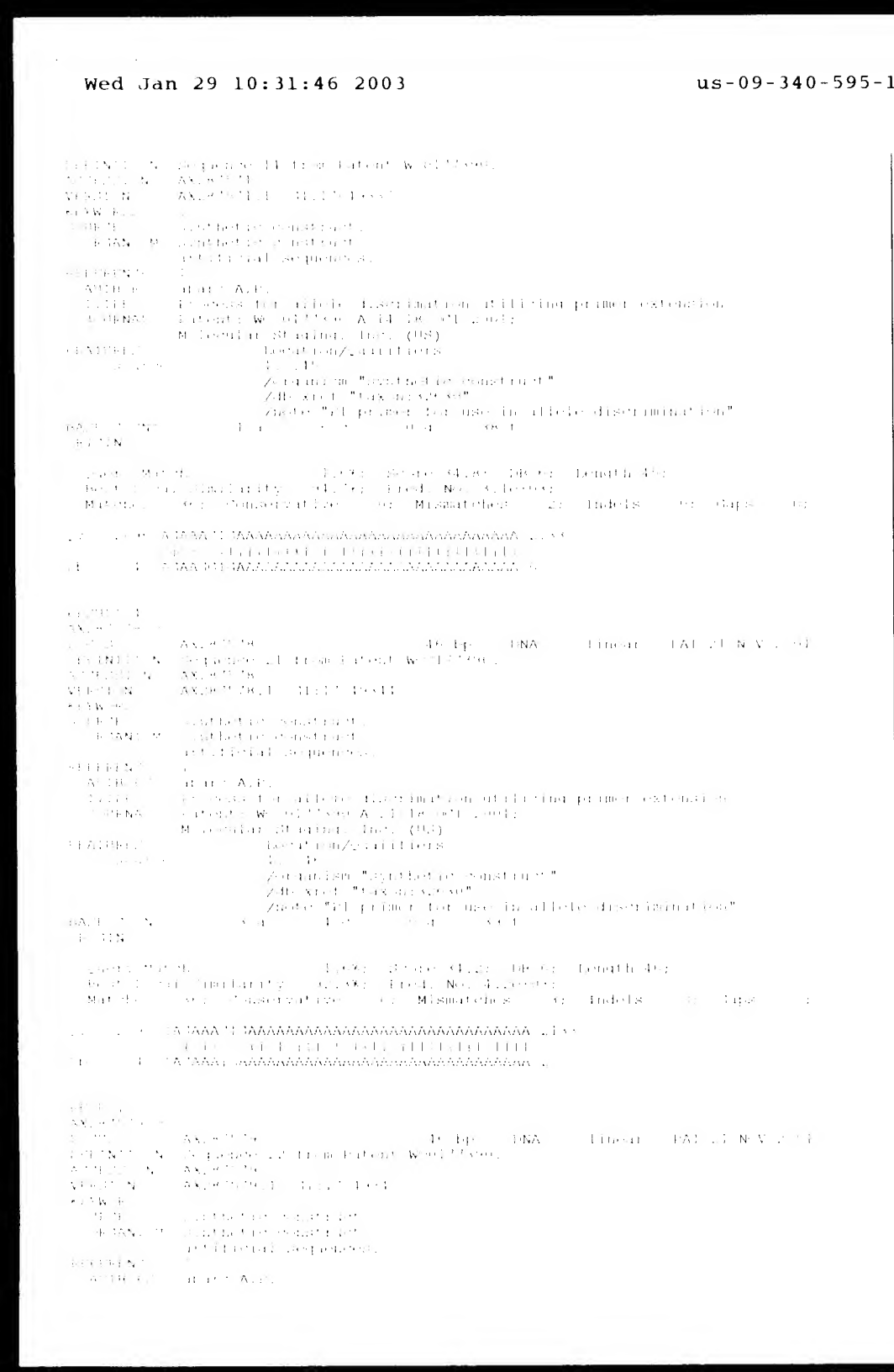

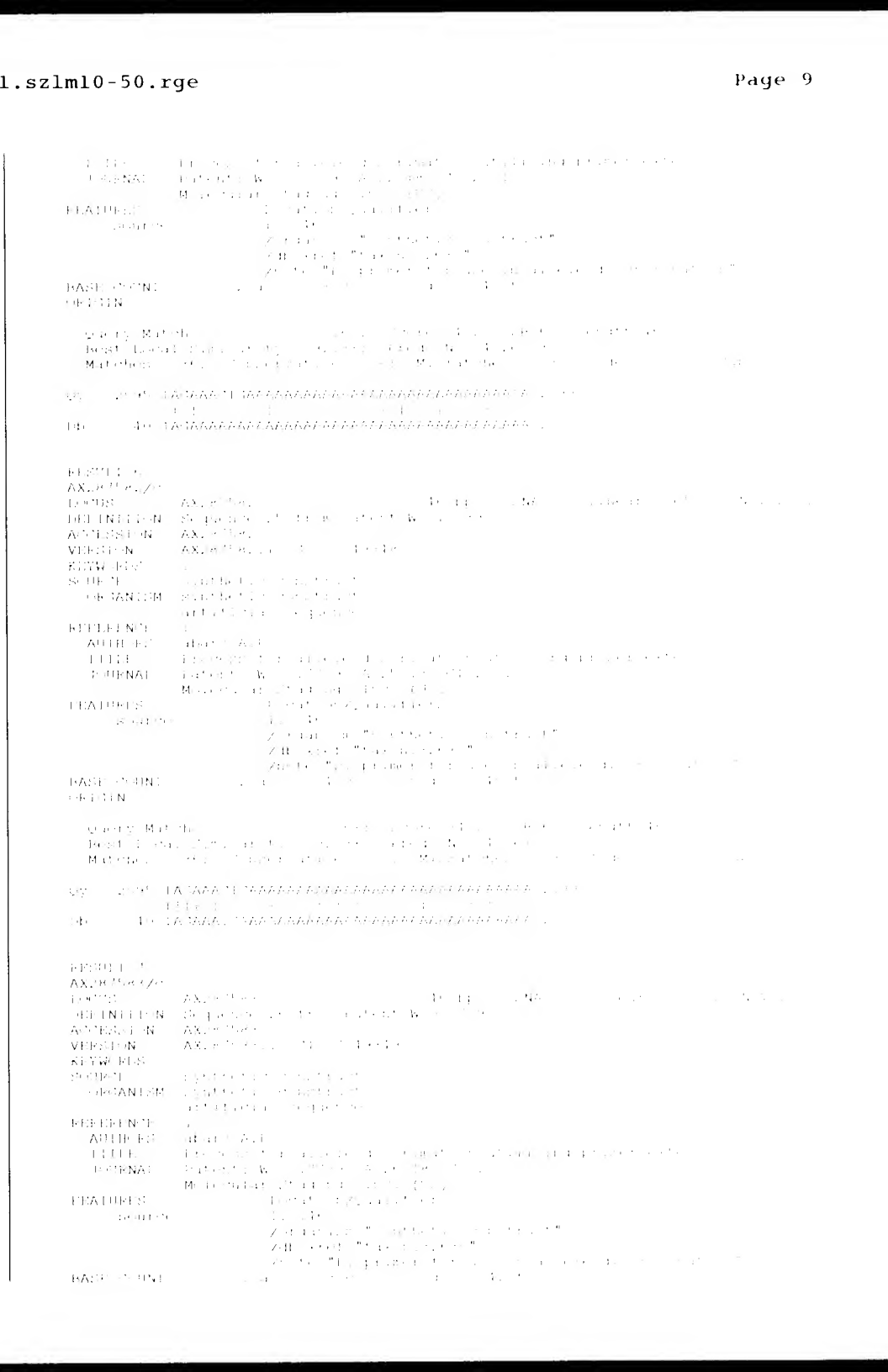

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RESULT 8
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DEFINITION  Sequence 9 from patent US 5807734.
ACCESSION   AR038858
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Jacobs,K., McCoy,J.M., LaVallie,E.R., Rivle,L.A., Merberg,D.,
            Ivary,M., Evans,C., Spaulding,V. and Freeman,M.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: US 5807734-A 9 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1..44
                     /organism="unknown"
BASE COUNT       43 a      0 c      1 g      0 t
ORIGIN

  Query Match             1.6%;  Score 33.2;  DB 6;  Length 44;
  Best Local Similarity   92.1%;  Pred. No. 7e-04;
  Matches   35;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2096 AGAAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
             | | |  ||||||||||||||||||||||||||||||||||||||
Db         7 AAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44

RESULT 9
AX261361/c
LOCUS       AX261361                  50 bp    DNA     linear   PAT 20-OCT-2001
DEFINITION  Sequence 1012 from Patent WO0173027.
ACCESSION   AX261361
VERSION     AX261361.1  GI:16716928
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Mezther,M.J., Xu,J. and Kiel,G.E.
  TITLE     Compositions and methods for therapy and diagnosis of [illegible] cancer
  JOURNAL   Patent: WO 0173027-A 1012 04-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       0 a      0 c      0 g     50 t
ORIGIN

  Query Match             1.5%;  Score 32.4;  DB 6;  Length 50;
  Best Local Similarity   78.0%;  Pred. No. 1.6e-04;
  Matches   39;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      2082 AAAAATGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
             |||| || |   | |||   ||||||||||||||||||||||||||||||||||||||
Db        50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 10
[illegible]
LOCUS       [illegible]                [illegible] bp    DNA     [illegible]
DEFINITION  Sequence [illegible] from patent [illegible].
ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Burwell,[illegible].
  TITLE     Fluorescent [illegible] [illegible] [illegible]
  JOURNAL   Patent: US [illegible]-A [illegible] [illegible]
FEATURES             Location/Qualifiers
     source          [illegible]
                     /[illegible]="[illegible]"
BASE COUNT       [illegible]
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 6;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Gaps    [illegible];

Qy      2082 AAAAATGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
             [illegible]
Db        [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]

RESULT 11
A48799
LOCUS       A48799                    [illegible] bp    DNA     [illegible]
DEFINITION  Sequence [illegible] from Patent W[illegible].
ACCESSION   A48799
VERSION     A48799.1  GI:[illegible]
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Petrik,J., Allain,J. and Reason,G.I.
  TITLE     OLIGONUCLEOTIDES AND [illegible] USE
  JOURNAL   Patent: WO [illegible]-A [illegible] [illegible]
            LYNXVALE LTD (IE)
COMMENT     [illegible] patent [illegible] [illegible]
FEATURES             Location/Qualifiers
     source          1..40
                     /[illegible]="[illegible]"
                     /db_xref="taxon:[illegible]"
BASE COUNT       40 a      0 c      0 g      0 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 6;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Gaps    [illegible];

Qy      2096 AGAAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
             | |||  ||  | |||  ||||||||||||||||||||||
Db        [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]

RESULT 12
AX225[illegible]/c
LOCUS       AX225[illegible]                [illegible] bp    DNA     [illegible]
DEFINITION  Sequence [illegible] from Patent W[illegible].
ACCESSION   AX225[illegible]
VERSION     AX225[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      [illegible]
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Schorer,J.E.
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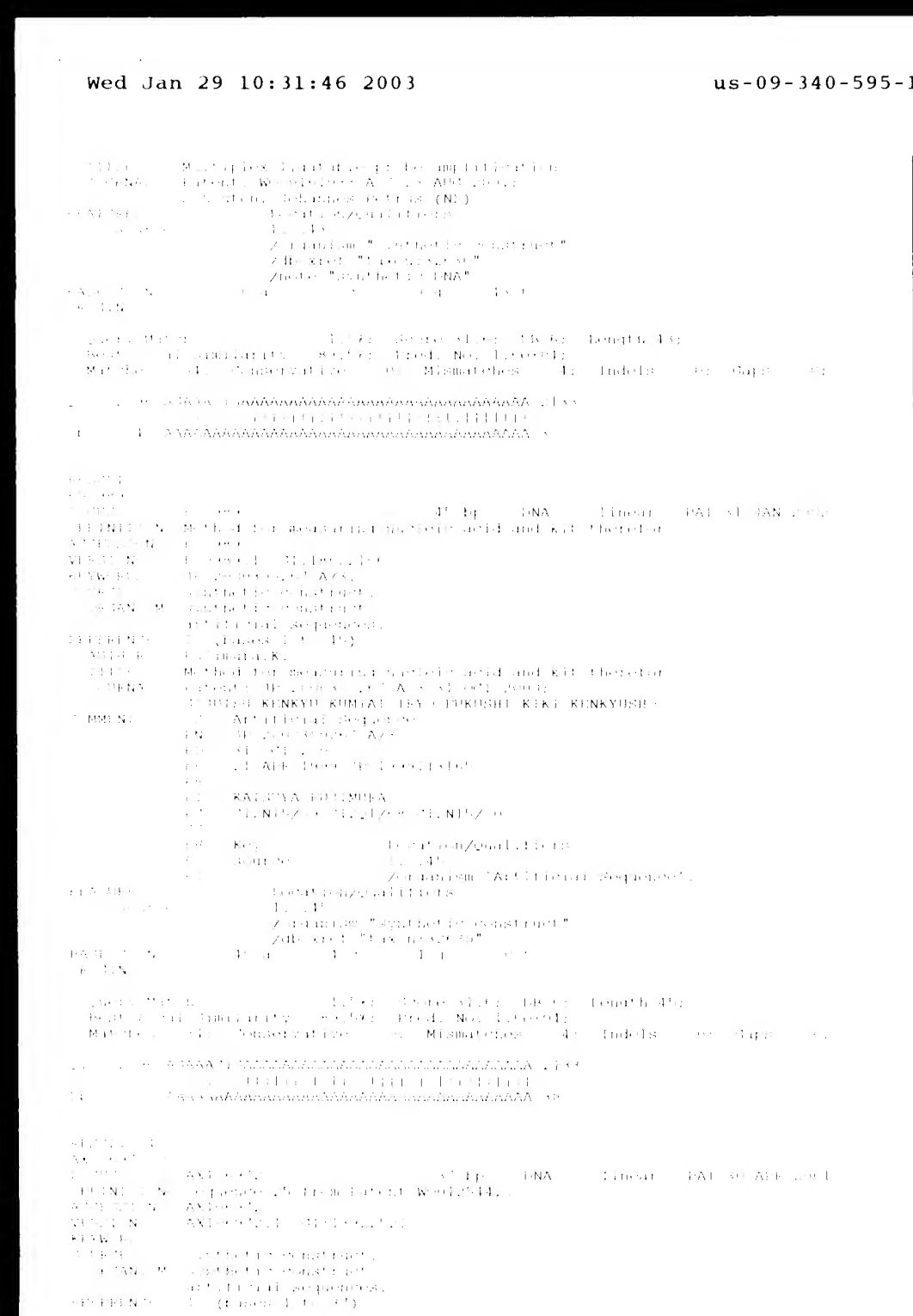

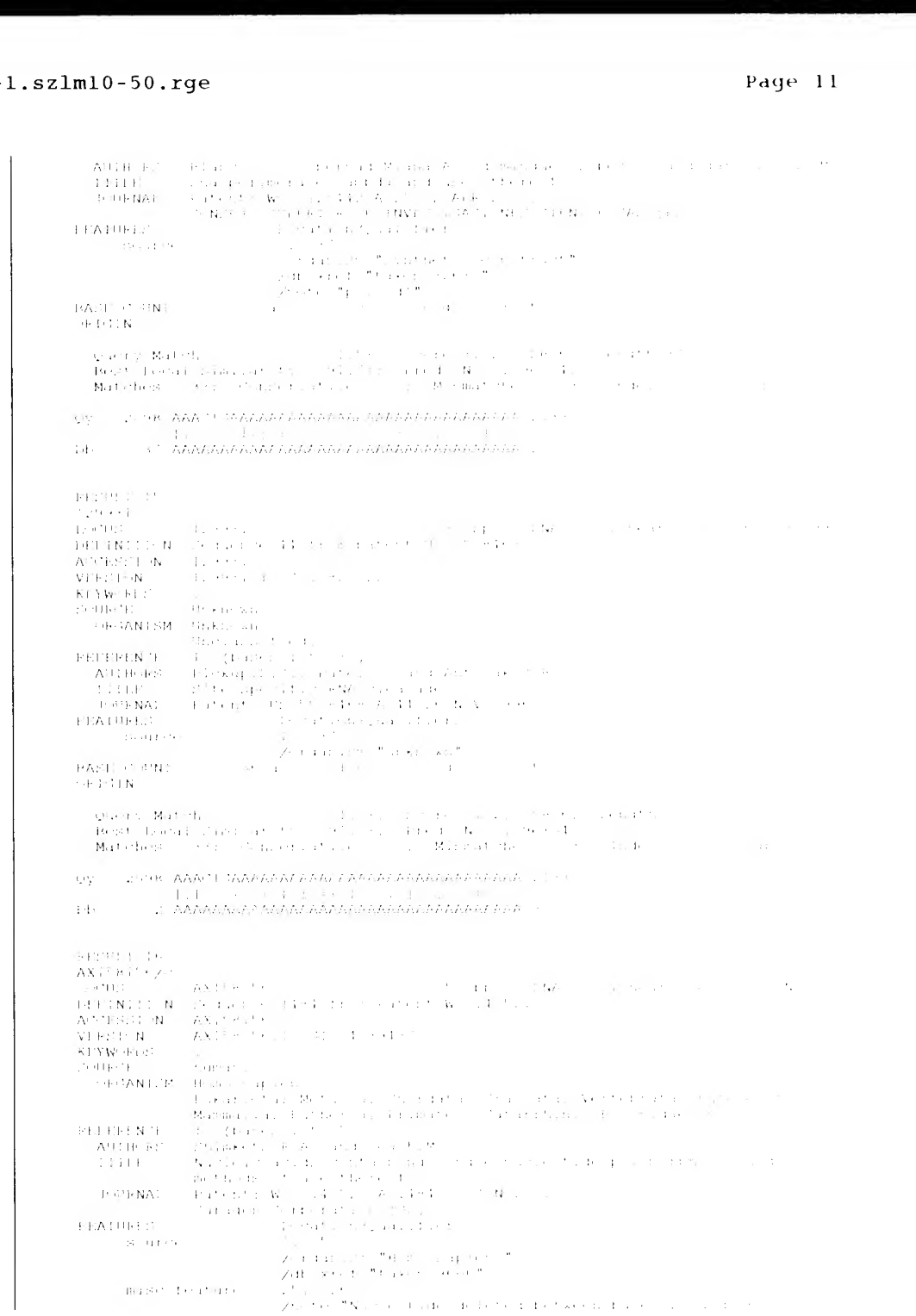

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                     Accession number AX287570."
     misc_feature    26
                     /note "2 or 3 allelic variants (1 is other strand)"
BASE COUNT        14 a      9 c      9 g     13 t
ORIGIN

  Query Match             1.5%;  Score 31.2;  DB 6;  Length 45;
  Best Local Similarity   81.5%;  Pred. No. 2e-04;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    1 GGGGAATTCATAAATTGAAAAAAAAAAAAAAAAAAAAAAAAA 45
          |||| || | ||| ||| |||||||| ||||||| |||||
Db     44 AATTCTCTAAAAAAGAAAAAAAAAAGAAAAAAAAAAAAAAA 1


RESULT 17
AX287570/c
LOCUS       AX287570                45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 13 from Patent WO0177390.
ACCESSION   AX287570
VERSION     AX287570.1  GI:17331566
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Abarzua,P.
  TITLE     Process for allele discrimination utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 13 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..45
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note "P1 primer for use in allele discrimination"
BASE COUNT        14 a      9 c      9 g     13 t
ORIGIN

  Query Match             1.4%;  Score 30.8;  DB 6;  Length 45;
  Best Local Similarity   94.1%;  Pred. No. 2.4e-04;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    0;

Qy    1 GGGGAATTCATAAATTGAAAAAAAAAAAAAAAAAAAAAAAAA 45
          | |||||||||||||||||||||||||||||||||||||
Db     44 AATTCTCTAAAAAAGAAAAAAAAAAGAAAAAAAAAAAAAA 1


RESULT 18
AX287574/c
LOCUS       AX287574                45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 17 from Patent WO0177390.
ACCESSION   AX287574
VERSION     AX287574.1  GI:17331570
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Abarzua,P.
  TITLE     Process for allele discrimination utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 17 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..45
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note "P1 primer for use in allele discrimination"
BASE COUNT        14 a      9 c      9 g     13 t
ORIGIN

  Query Match             1.4%;  Score 30.8;  DB 6;  Length 45;
  Best Local Similarity   94.1%;  Pred. No. 2.4e-04;
  Matches   32;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    0;

Qy    1 GGGGAATTCATAAATTGAAAAAAAAAAAAAAAAAAAAAAAAA 45
          | |||||||||||||||||||||||||||||||||||||
Db     44 AATTCTCTAAAAAAGAAAAAAAAAAGAAAAAAAAAAAAAA 1


RESULT 19
AX166869/c
LOCUS       AX166869                45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 5 from Patent WO0177390.
ACCESSION   AX166869
VERSION     AX166869.1  GI:14572347
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Brentano,S.T., Jucket,M.I., Delgado,F.M., Closziat,...
            Rodriguez,M.
  TITLE     Nucleic acid amplification and detection of mycobacterium species
  JOURNAL   Patent: WO 0177390-A 5 18-OCT-2001;
            Gen-Probe Incorporated (US) ; Biogenerix S.A. (ES)
FEATURES             Location/Qualifiers
     source          1..45
                     /organism="mycobacterium avium"
                     /db_xref="taxon:1764"
                     /note="capture oligo"
     modified_base   1
                     /mod_base=m
     modified_base   2
                     /note="2'-O-methoxy oligonucleo"
                     /mod_base=OMeA
     modified_base   3
                     /note="2'-O-methoxy oligonucleo"
                     /mod_base=OMeA
     modified_base   4
                     /mod_base=m
     modified_base   5
                     /note="2'-O-methoxy oligonucleo"
                     /mod_base=OMeA
     modified_base   6
                     /mod_base=m
     modified_base   7
                     /note="2'-O-methoxy oligonucleo"
                     /mod_base=OMeA
     modified_base   8
                     /mod_base=m
     modified_base   9..11
                     /mod_base=m
     modified_base   12
                     /mod_base=A
     modified_base   13
                     /note="2'-O-methoxy oligonucleo"
                     /mod_base=OMeA
     modified_base   14
                     /note="2'-O-methoxy oligonucleo"
                     /mod_base=OMeA
     modified_base   15
                     /note="2'-O-methoxy oligonucleo"
                     /mod_base=OMeA
BASE COUNT        [illegible]
ORIGIN

  Query Match             [illegible]  Score [illegible]  DB 6;  Length 45;
  Best Local Similarity   [illegible]  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches    4;  Indels    [illegible];  Gaps    [illegible]

Qy    2 GGGAATTCATAAATTGAAAAAAAAAAAAAAAAAAAAAAAAA 45
          | | |||||||||| | |||||  | |||| | ||||
Db     44 TCTCTAAAAAAGAAAAAAAAAAGAAAAAAAAAAAAAAAAA 48


RESULT 20
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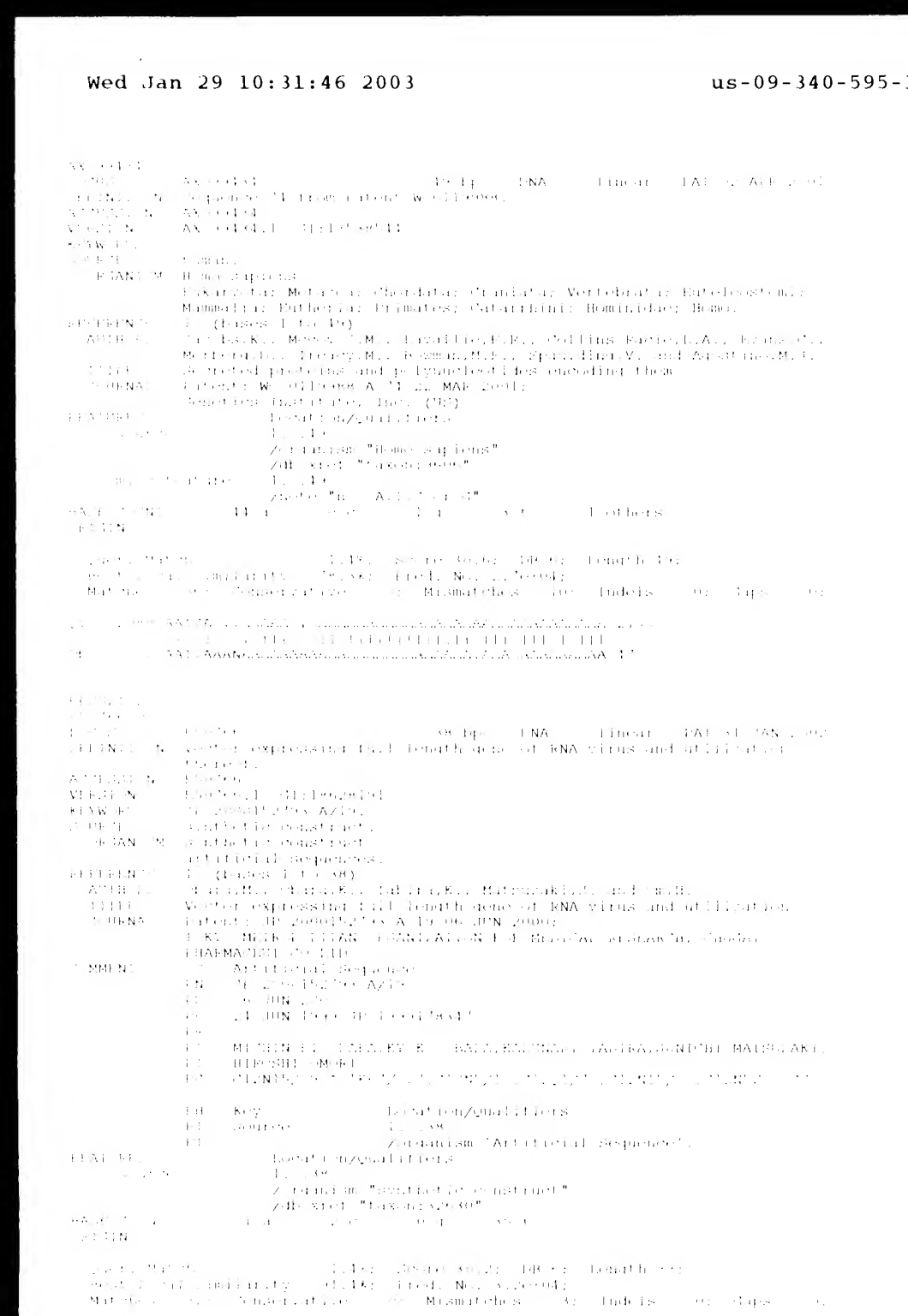

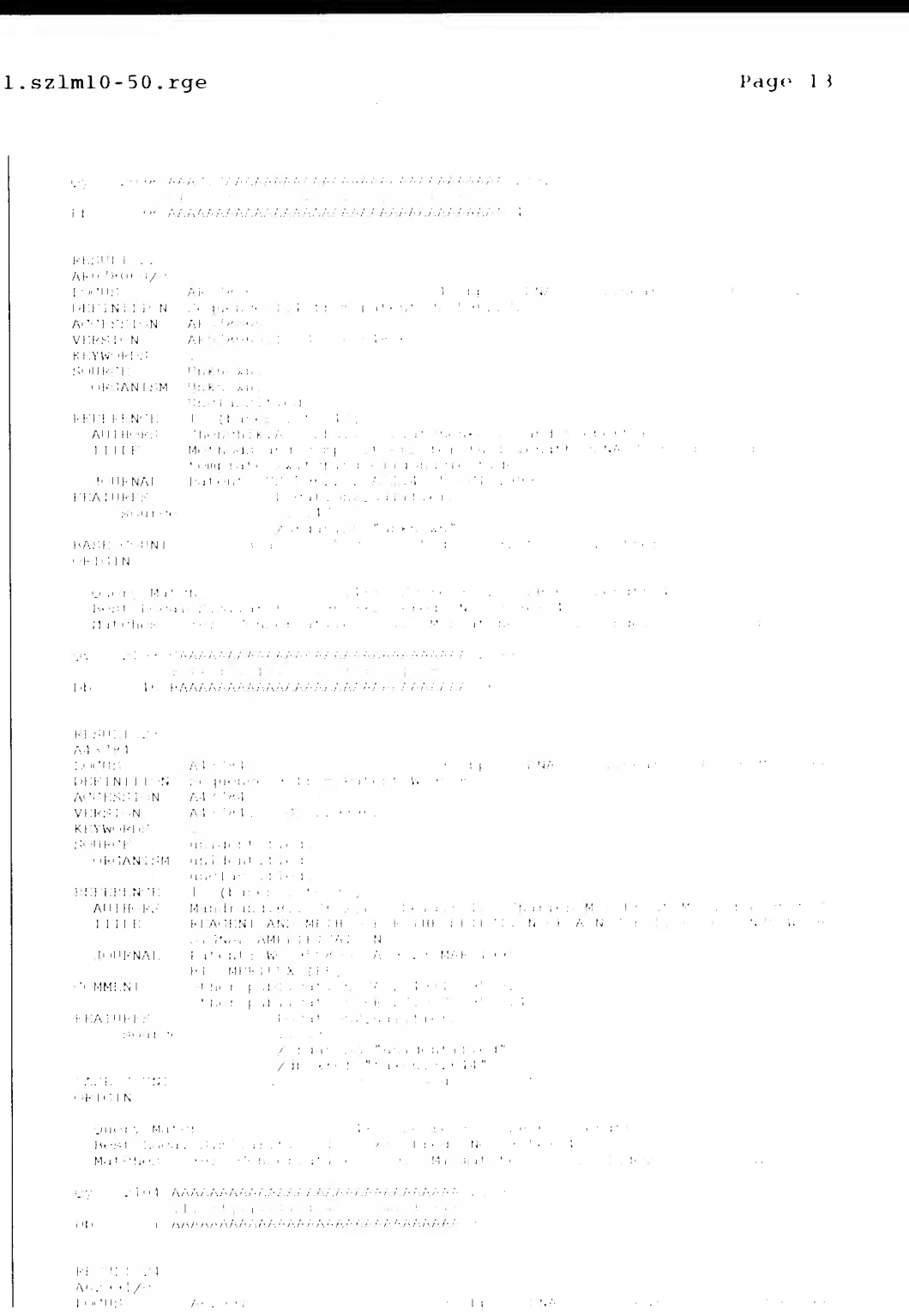

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DEFINITION  Sequence 1 from Patent WO9720063.
ACCESSION   A62994
VERSION     A62994.1  GI:3719867
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720063 A 5 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT         9 a        0 c        0 g       30 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30
          ||||||||||||||||||||||||||||||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 25
A62995
LOCUS       A62995                    30 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 7 from Patent WO9720063.
ACCESSION   A62995
VERSION     A62995.1  GI:3719867
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720063 A 5 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unidentified"
                     /db_xref="taxon:2711"
BASE COUNT        30 a        0 c        0 g        0 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
          ||||||||||||||||||||||||||||||
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30


RESULT 26
AR179066/c
LOCUS       AR179066                  30 bp    DNA     linear   PAT 16-MAY-2002
DEFINITION  Sequence 3 from patent US 6426144.
ACCESSION   AR179066
VERSION     AR179066.1  GI:20226621
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     Method for generating multiple double stranded nucleic acids
  JOURNAL   Patent: US 6426144 A 3 23-JUL-2002;
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT         9 a        0 c        0 g       30 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30
          ||||||||||||||||||||||||||||||
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 27
AR179070
LOCUS       AR179070                  30 bp    DNA     linear   PAT 16-MAY-2002
DEFINITION  Sequence 7 from patent US 6426144.
ACCESSION   AR179070
VERSION     AR179070.1  GI:20226625
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     Method for generating multiple double stranded nucleic acids
  JOURNAL   Patent: US 6426144 A 7 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unidentified"
BASE COUNT        30 a        0 c        0 g        0 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
          ||||||||||||||||||||||||||||||
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30


RESULT 28
AX104902/c
LOCUS       AX104902                  30 bp    DNA     linear   PAT 04-JUN-2002
DEFINITION  Sequence 1 from patent WO 02/
ACCESSION   AX104902
VERSION     AX104902.1  GI:19021099
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kriegler,M., Schoenberger, and Voss,T.
  TITLE     Improved regular expression matching
  JOURNAL   Patent: WO 02/072-A 12-SEP-2002;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); CORIXA CORPORATION
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1..30
                     /note="Description of Sequence"
                     /db_xref="taxon:32644"
                     /mol_type="Sequence"
BASE COUNT         9 a        0 c        0 g       21 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30
```

```
RESULT 33
I8445
LOCUS       I8445o                    30 bp    DNA     linear   PAT 11 APR 1998
DEFINITION  Sequence 9 from patent US 5695936.
ACCESSION   I8445o
VERSION     I8445o.1  GI:3921979
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Mandrand,B., Cros,P., Delair,T., Charles,M.-H., Erout,M.-N. and
            Pichot,C.
  TITLE     Reagent and method for the detection of a nucleotide sequence with
            signal amplification
  JOURNAL   Patent: US 5695936-A 9 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1..30
                     /organism="unknown"
BASE COUNT       30 a      0 c      0 g      0 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
              ||||||||| |||||||||| | ||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30


RESULT 34
AR099615/c
LOCUS       AR099615                  33 bp    DNA     linear   PAT 14 FEB 2001
DEFINITION  Sequence 29 from patent US 6077934.
ACCESSION   AR099615
VERSION     AR099615.1  GI:12809381
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
  TITLE     Contryphan peptides
  JOURNAL   Patent: US 6077934-A 26 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="unknown"
BASE COUNT        0 a      1 c      2 g     30 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
              ||| ||||||||||||||| ||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4


RESULT 35
AR120128/c
LOCUS       AR120128                  33 bp    DNA     linear   PAT 16 MAY 2001
DEFINITION  Sequence 26 from patent US 6153738.
ACCESSION   AR120128
VERSION     AR120128.1  GI:14112827
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
  TITLE     Contryphan peptides
  JOURNAL   Patent: US 6153738-A 26 28-NOV-2000;
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="unknown"
BASE COUNT        0 a      1 c      2 g     30 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
              |||||||||||||||| ||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4


RESULT 36
BD011883/c
LOCUS       BD011883                  33 bp    DNA     linear   PAT [illegible]
DEFINITION  Detection kit for SRSV.
ACCESSION   BD011883
VERSION     BD011883.1  GI:[illegible]
KEYWORDS    WO [illegible] A/13.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Takeda,N., Natori,K., Miyamura,T., Kamata,K., Sato,S. and
            Sato,S.
  TITLE     Detection kit for SRSV
  JOURNAL   Patent: WO [illegible] A 13 28-DEC-2000;
            JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE
            OF INFECTIOUS DISEASES, DENKA SEIKEN CO LTD; NAKAYA
            TAKEDA, KAZUHIKO NATORI, TATSUO MIYAMURA, KUNIO KAMATA, SHUNICHI
            SATO, SEIYA SATO
COMMENT     OS   Artificial Sequence
            PN   WO [illegible] A/13
            PD   28-DEC-2000
            PF   22-JUN-2000 WO [illegible]
            PR   22-JUN-1999 JP [illegible]
            PI   NAOKAZU TAKEDA, KAZUHIKO NATORI, TATSUO MIYAMURA, KUNIO
            KAMATA, SHUNICHI SATO,
            PI   SEIYA SATO
            PC   C12N15/56, C12N15/40
            CC
            FH   Key             Location/Qualifiers
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        0 a      0 c      0 g     33 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
              ||| ||||||||||||||| |||| ||||
Db         32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3


RESULT 37
BD004364/c
ID   BD004364  standard; DNA; SYN;  33
XX
AC   BD004364;
XX
SV   BD004364.1
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```
XX
DT   [illegible] (Rel. [illegible] Created)
DT   [illegible] (Rel. [illegible] Last updated, Version [illegible])
XX
DE   [illegible] kit for SRSV.
XX
KW   [illegible] 1Z1[illegible].
XX
OS   [illegible] construct
OS   artificial sequence.
XX
PN   [illegible]
PD   [illegible]
PA   [illegible] N., Natori K., Miyamura [illegible], Kamata K., Sa[illegible], Sato S.;
PT   "[illegible] kit for SRSV";
PT   Patent number [illegible] 1Z1[illegible] [illegible] JAN 2001.
PS   NA[illegible] NAT INST OF INFECTIOUS DISEASE.
XX
CC   [illegible] Artificial Sequence
CC   PN  [illegible] 1Z1[illegible]
CC   [illegible] JAN 2001
CC   [illegible] JUN 2000 [illegible]
CC   [illegible] JUN 1999 [illegible]
CC   [illegible] NA[illegible] TAKEDA [illegible] NAT[illegible] MIYAMURA,KUNI[illegible] KAMATA.
CC   [illegible] [illegible]KI SAT[illegible]
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CC   [illegible] [illegible]ZI[illegible]
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CC   [illegible]   [illegible]
CC   [illegible]   /organism "Artificial Sequence"
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FT                /db_xref "[illegible]"
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XX
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Qy     [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]
           [illegible]
Db     [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]


RESULT [illegible]
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DEFINITION  Sequence [illegible] from Patent W[illegible].
ACCESSION   A[illegible]
VERSION     A[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   [illegible] (bases 1 to [illegible])
  AUTHORS   [illegible]
  TITLE     [illegible] CLASS OF [illegible]NUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTI[illegible]
            AGENTS
  JOURNAL   Patent: W[illegible] A [illegible] JUN [illegible];
            [illegible] (US)
COMMENT     Other publication [illegible]
            Other publication [illegible]
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ORIGIN

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Qy     [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]
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Db     [illegible] AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]


RESULT [illegible]
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DEFINITION  Sequence [illegible] from patent [illegible]
ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   [illegible]
  AUTHORS   [illegible]
  TITLE     [illegible]
            [illegible]
  JOURNAL   Patent: [illegible]
FEATURES             Location/Qualifiers
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BASE COUNT  [illegible]
ORIGIN

  Query Match          [illegible]
  Best Local Similarity   [illegible]
  Matches  [illegible]  Mismatches  [illegible]

Qy     2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]
           [illegible]
Db       42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]


RESULT 1[illegible]
AX[illegible]
LOCUS       AX[illegible]    [illegible]    DNA    [illegible]
DEFINITION  Sequence [illegible] from Patent W[illegible]
ACCESSION   AX[illegible]
VERSION     AX[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      [illegible]
  ORGANISM  [illegible]
            [illegible]
REFERENCE   [illegible]
  AUTHORS   [illegible]
            [illegible]
  TITLE     [illegible]
            [illegible]
  JOURNAL   Patent: W[illegible]
            A[illegible]
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism "[illegible]"
                     /db_xref "[illegible]"
                     /note "[illegible]"
BASE COUNT  [illegible]
ORIGIN

  Query Match          [illegible]
  Best Local Similarity   [illegible]
  Matches  [illegible]

Qy     2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]
           [illegible]
Db        1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]
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RESULT 11
AX443022/c
LOCUS       AX443022                  43 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 1485 from Patent WO0214361.
ACCESSION   AX443022
VERSION     AX443022.1  GI:21690510
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Raitano,A.B., Challita-Eid,P.M., Faris,M., Saffran,D.C., Afar,D.E.,
            Levin,E., Hubert,R.S., Ge,W. and Jakobovits,A.
  TITLE     Nucleic acids and corresponding proteins entitled 83p2h3 and
            catrf2c11 useful in treatment and detection of cancer
  JOURNAL   Patent: WO 0214361 A 1485 21-FEB-2002;
            Agensys, Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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BASE COUNT        3 a      2 c      2 g     36 t
ORIGIN

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Qy    2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           ||||||||||||||||||||||||||||||
Db      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 14


RESULT 12
AX459616/c
LOCUS       AX459616                  43 bp    DNA     linear   PAT 08-NOV-2002
DEFINITION  Sequence 714 from Patent WO0218579.
ACCESSION   AX459616
VERSION     AX459616.1  GI:21725500
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Raitano,A.B., Faris,M., Hubert,R.S., Afar,D., Ge,W.,
            Challita-Eid,P. and Jakobovits,A.
  TITLE     Nucleic acid and corresponding protein entitled 85p1b3 useful in
            treatment and detection of cancer
  JOURNAL   Patent: WO 0218579 A 714 07-MAR-2002;
            Agensys, Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        3 a      2 c      2 g     36 t
ORIGIN

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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           ||||||||||||||||||||||||||||||
Db      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 14


RESULT 43
AX206861/c
LOCUS       AX206861                  44 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 7 from Patent WO0155391.
ACCESSION   AX206861
VERSION     AX206861.1  GI:15644085
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Jakobovits,A., Afar,D.E., Challita-Eid,P.M., Lacroix,
            Mitchell,S.C. and Hubert,R.S.
  TITLE     84p2a9: a prostate and testis specific protein highly expressed in
            prostate cancer
  JOURNAL   Patent: WO 0155391 A 7 02-AUG-2001;
            Urogenesys, Inc. (US)
FEATURES             Location/Qualifiers
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BASE COUNT        3 a      2 c      2 g     37 t
ORIGIN

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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           ||||||||||||||||||||||||||||||
Db      44 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 15


RESULT 44
I29927
LOCUS       I29927                    44 bp    DNA     linear   PAT 14-FEB-1997
DEFINITION  Sequence 49 from patent US 5578468.
ACCESSION   I29927
VERSION     I29927.1  GI:1827716
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Pickup,D.J., Patel,D. and Ashburner,J.L.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468 A 49 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1..44
                     /organism="unknown"
BASE COUNT       36 a      2 c      1 g      5 t
ORIGIN

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  Best Local Similarity   96.8%;  Pred. No. 3.7e-04;
  Matches   29;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy    2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           ||| | |||||||||||||||||||||||||||
Db      44 AAA-AAAAAAAAAAAAAAAAAAAAAAAAAA 45


RESULT 45
AX458031/c
LOCUS       AX458031                  47 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 23 from Patent WO0246387.
ACCESSION   AX458031
VERSION     AX458031.1  GI:21723483
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Warner,S., Hawkes,T. and Andrews,J.
  TITLE     Plant derived hydroxy phenyl pyruvate dioxygenases (hpd's) tolerant
            against triketone herbicides and transgenic plants containing such
```

```
  Query Match             1.4%;  Score 30;  DB 6;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+04;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           ||||||||||||||||||||||||||||||
Db      50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


RESULT 50
I28359/c
LOCUS       I28359                    50 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 5 from patent US 5571675.
ACCESSION   I28359
VERSION     I28359.1  GI:1819135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Baker,K., Chien,K., Kley,N., Pennica,D. and Wood,W.
  TITLE     Detection and amplification of cardiotrophin-1(cardiac hypertrophy
            factor)
  JOURNAL   Patent: US 5571675-A 5 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1..50
                     /organism "unknown"
BASE COUNT        3 a      7 c      7 g     33 t
ORIGIN

  Query Match             1.4%;  Score 30;  DB 6;  Length 50;
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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
           ||||||||||||||||||||||||||||||
Db      50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 21


Search completed: January 27, 2003, 09:23:58
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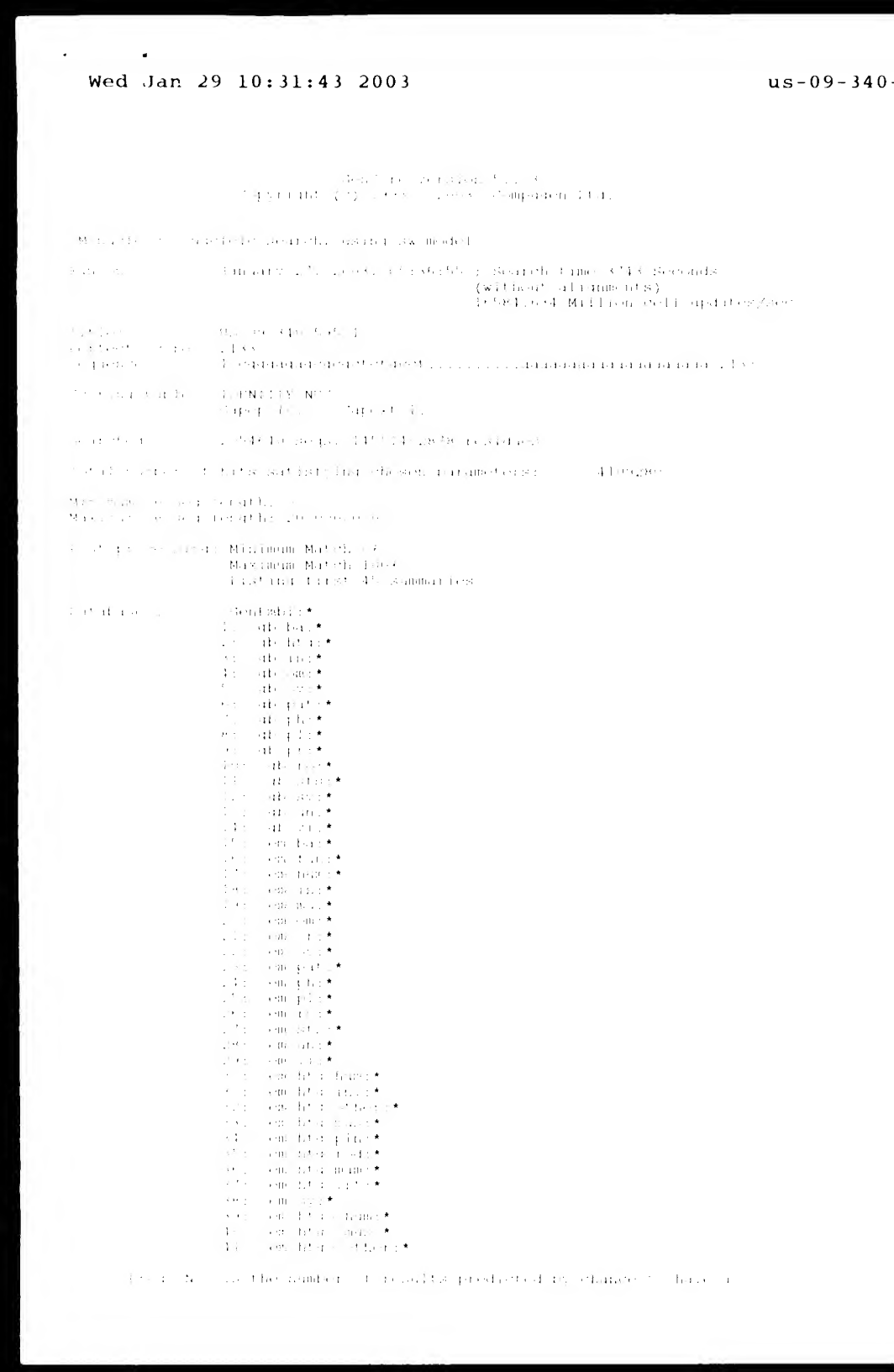

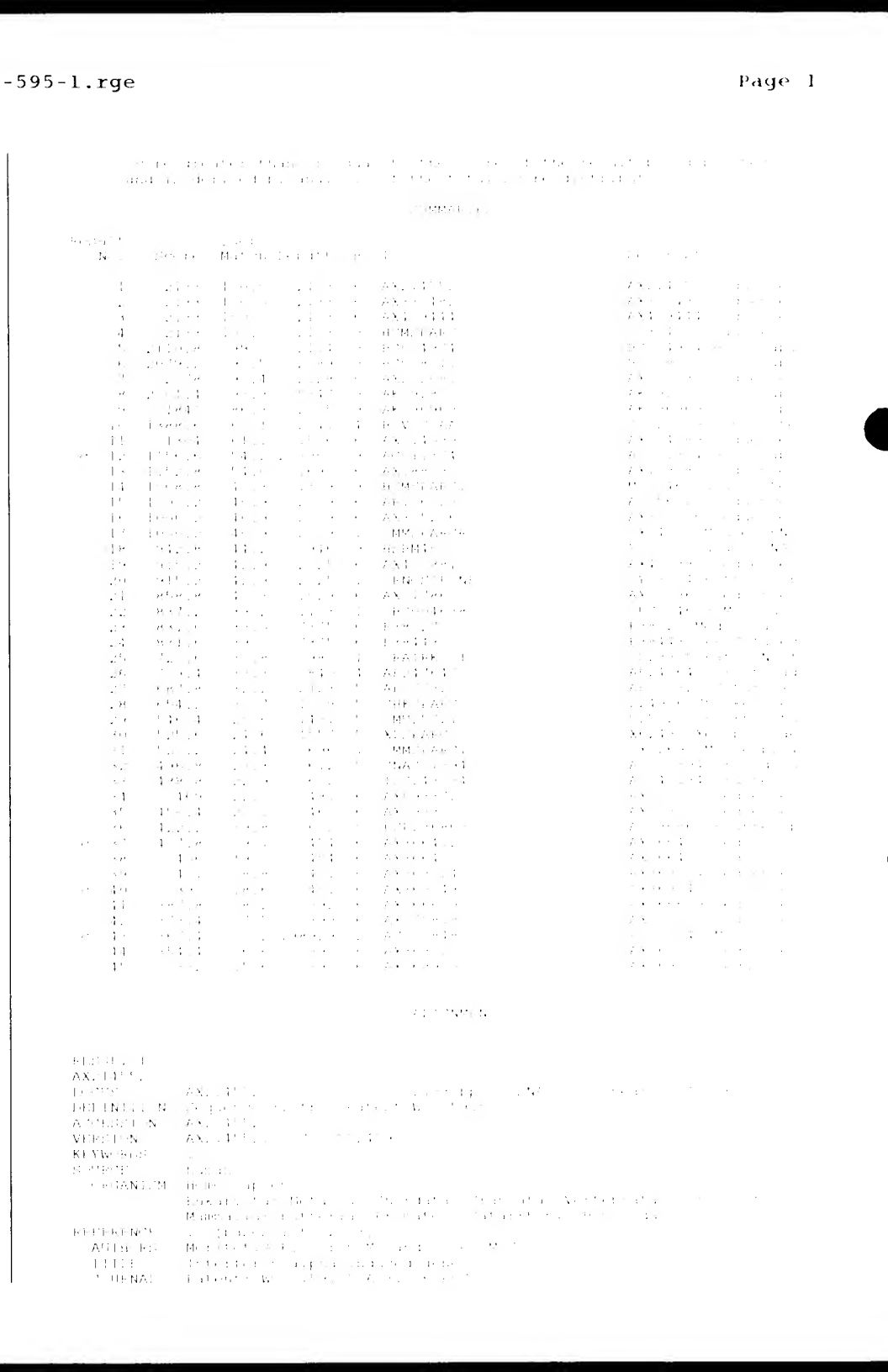

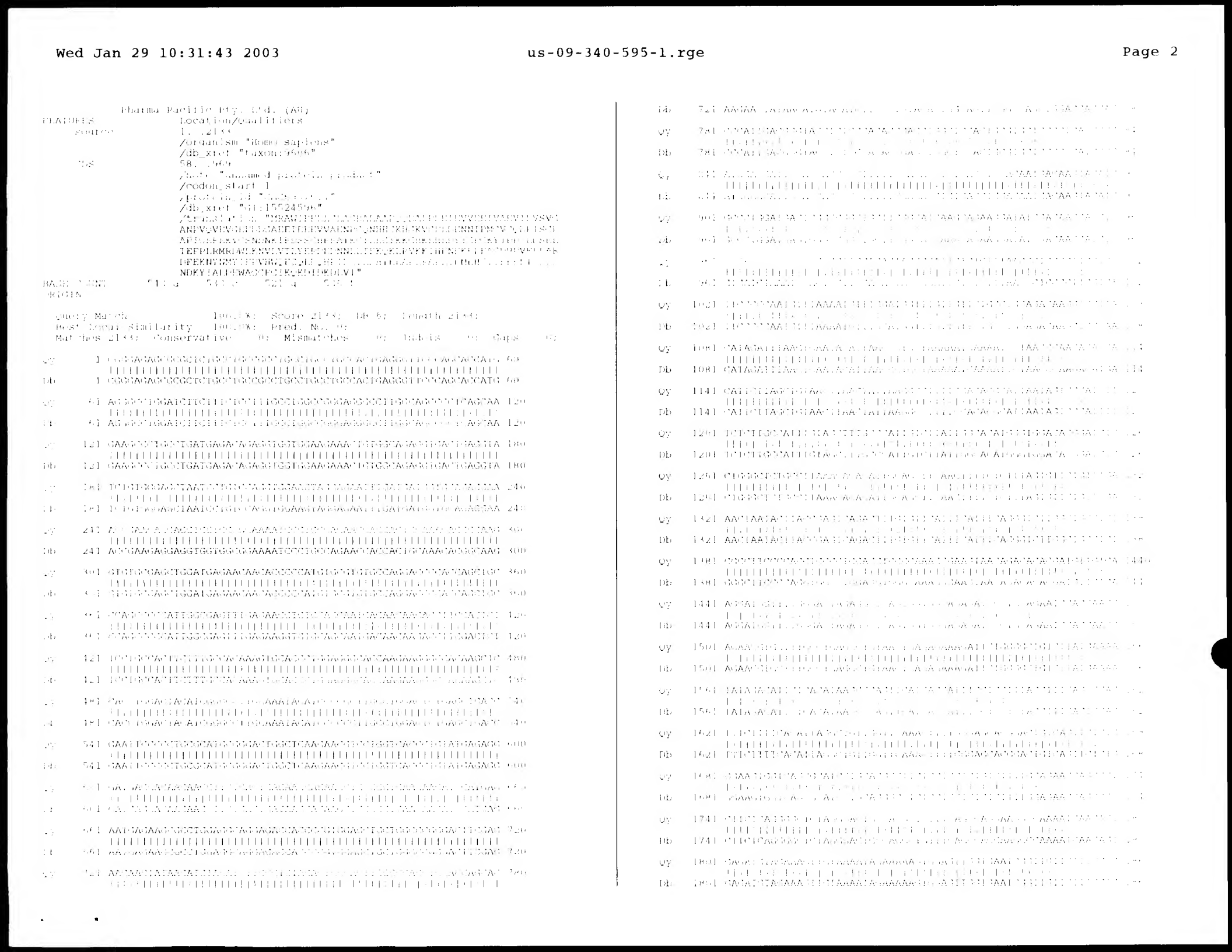

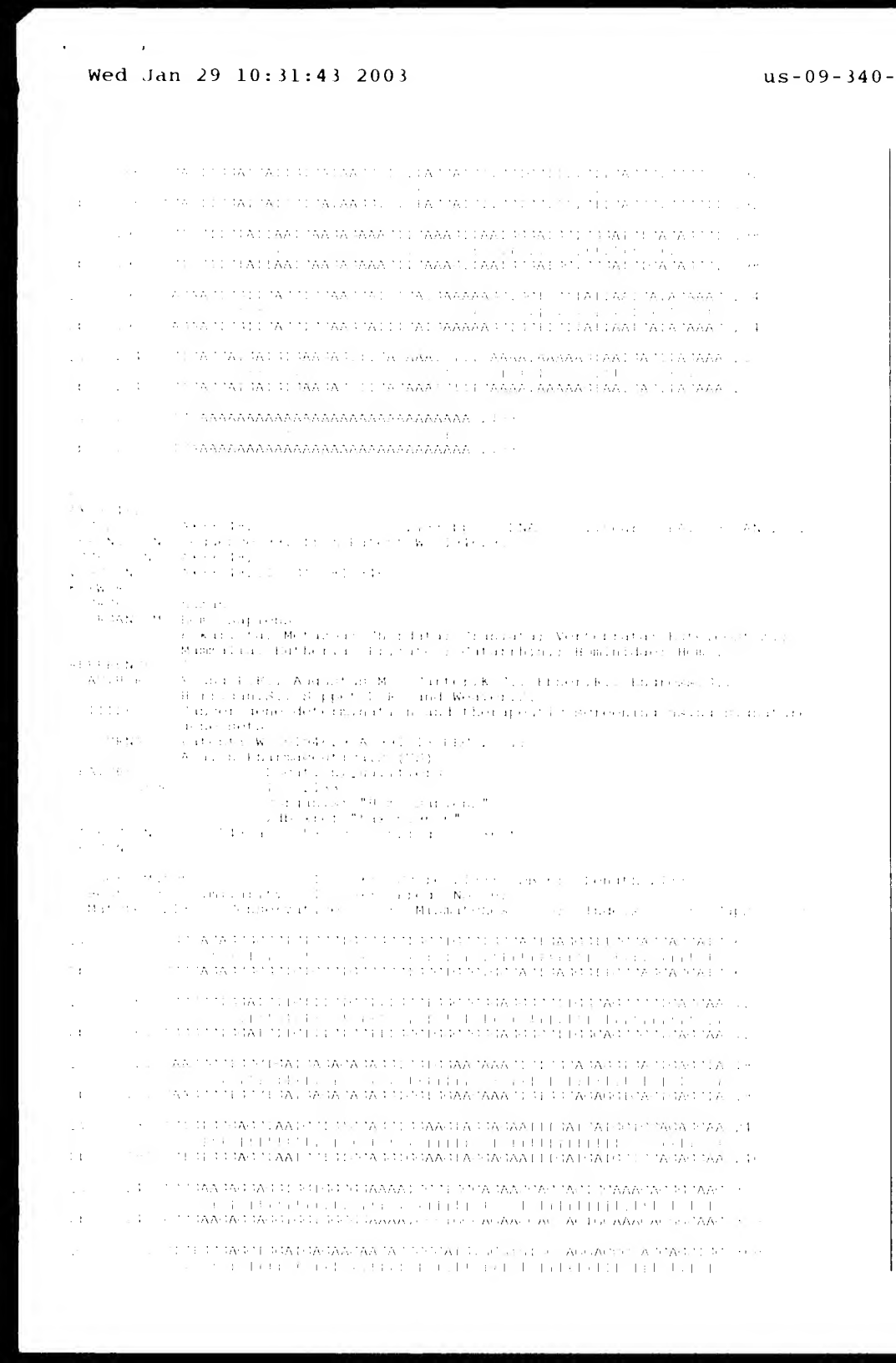

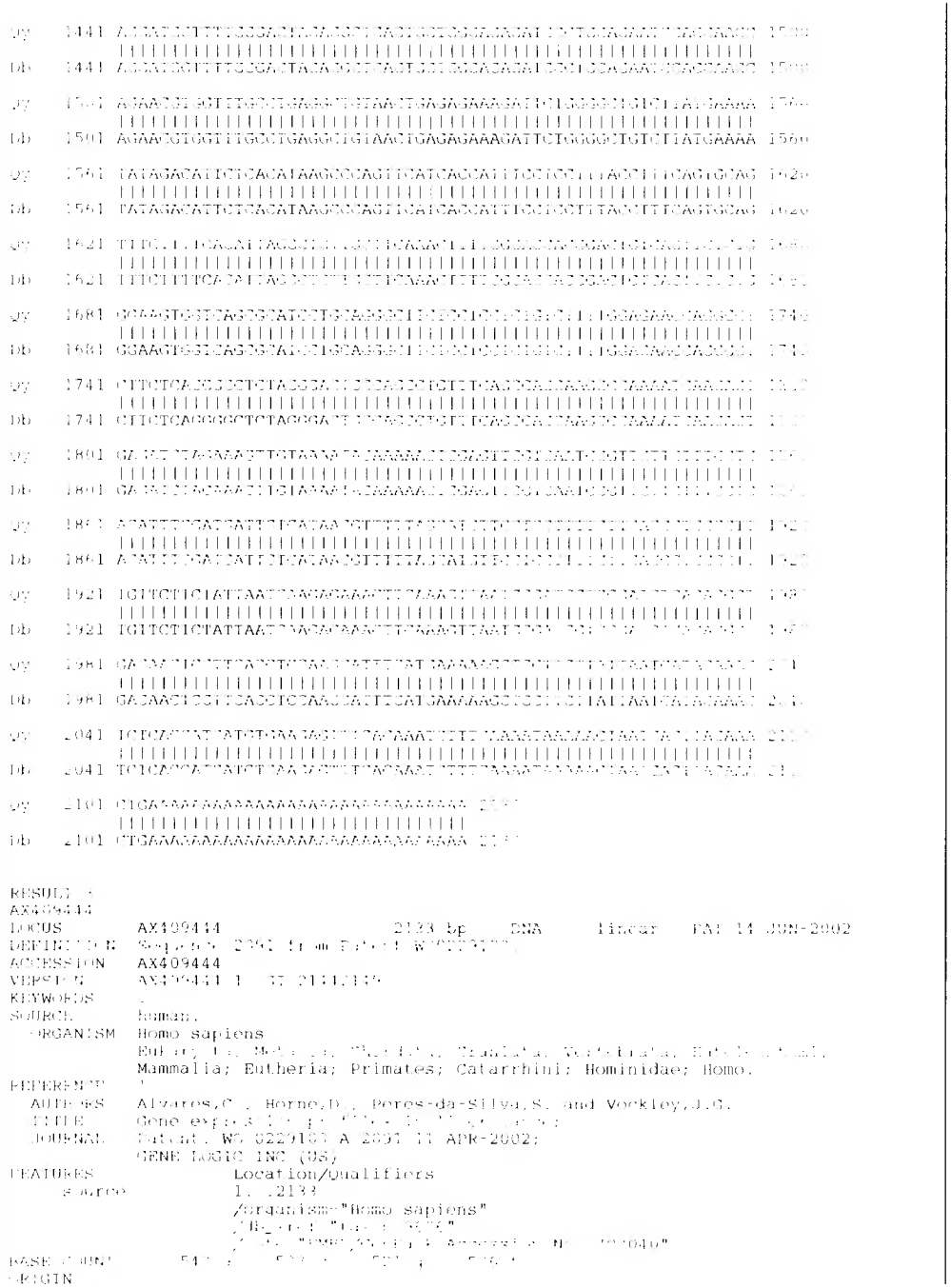

RESULT 1
AX409444
LOCUS AX409444 2133 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2942 from Patent WO0229107.
ACCESSION AX409444
VERSION AX409444.1 GI:21411439
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Alvaros,C., Horno,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE Gene expression [illegible]
JOURNAL Patent: WO 0229107 A 2001 11-APR-2002;
GENE LOGIC INC (US)
FEATURES Location/Qualifiers
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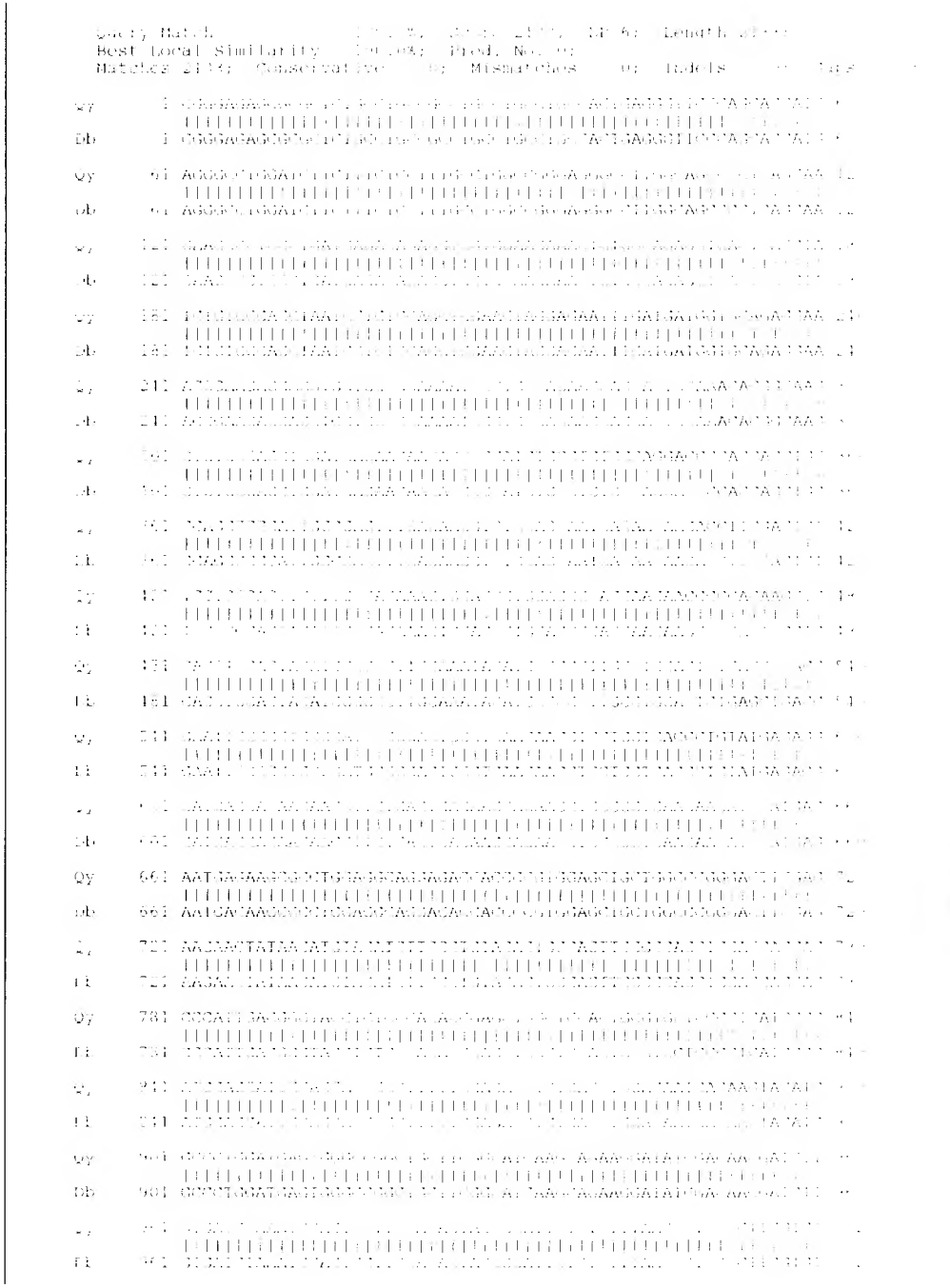
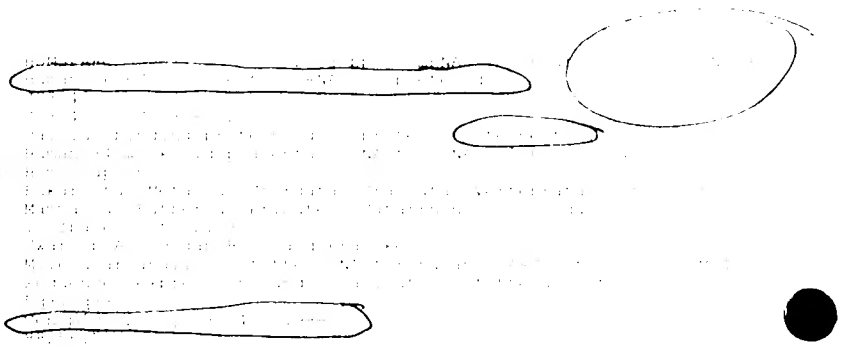
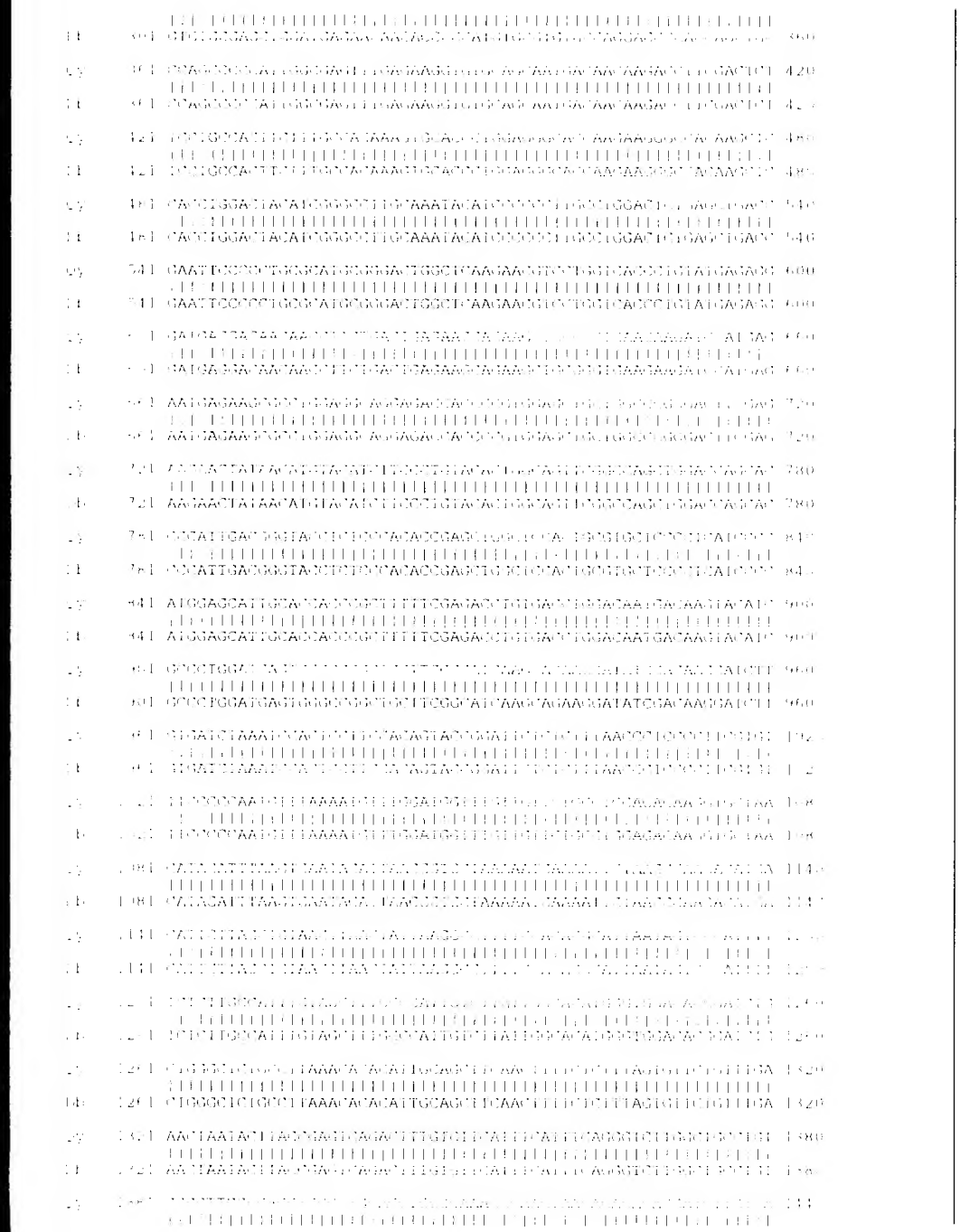
BASE COUNT 541 a 532 c 532 g 528 t
ORIGIN







RESULT 5
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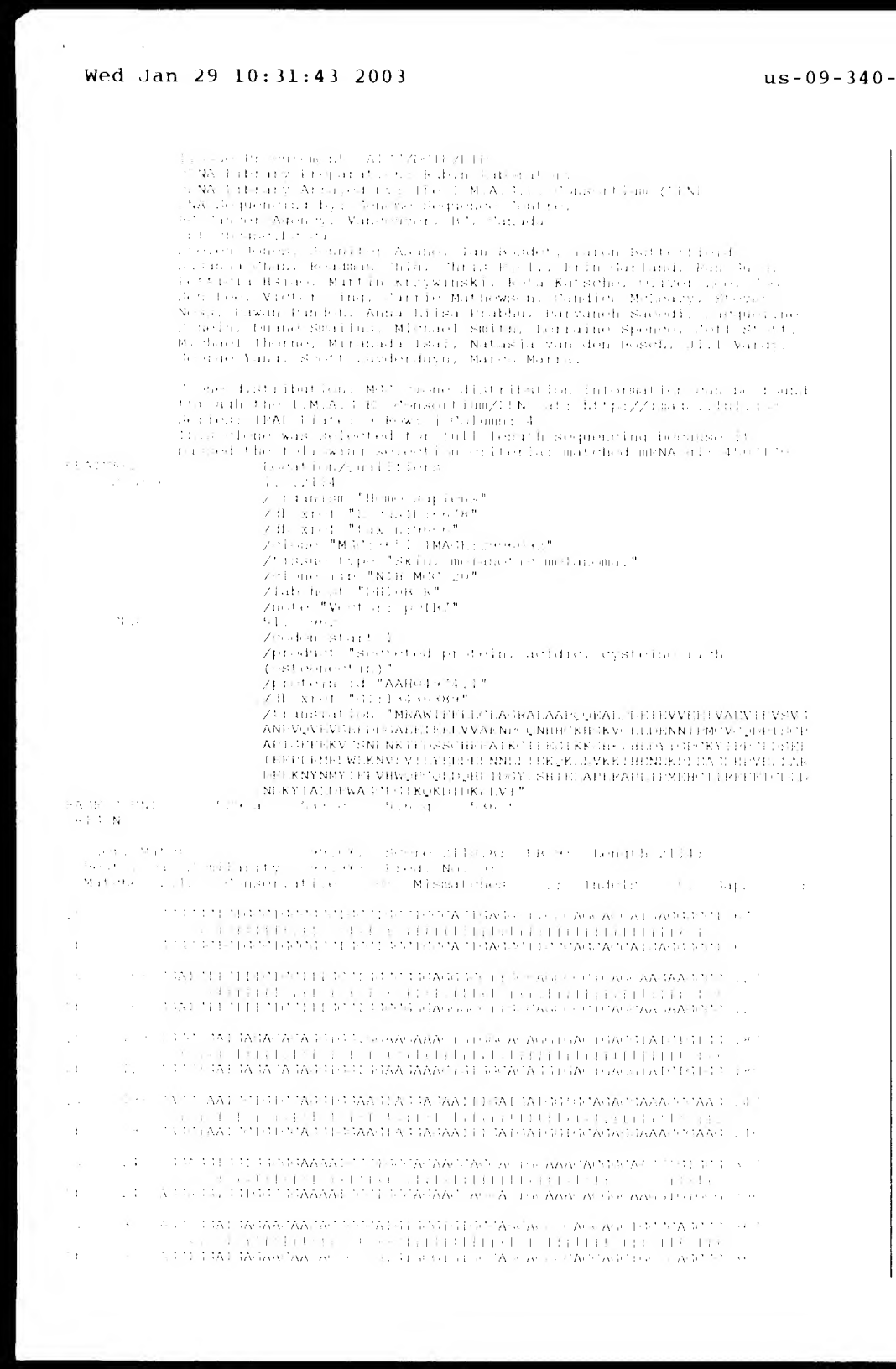
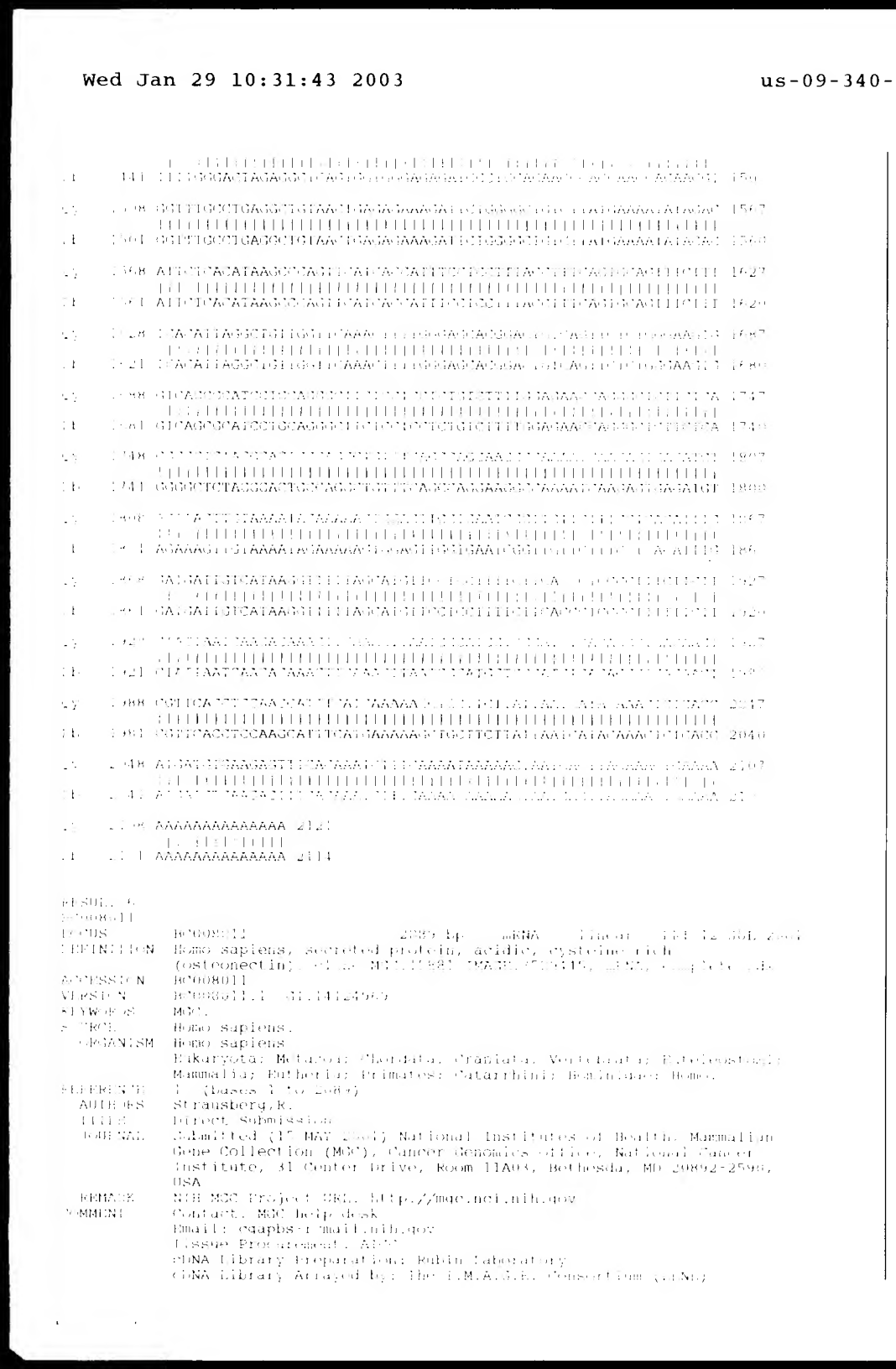
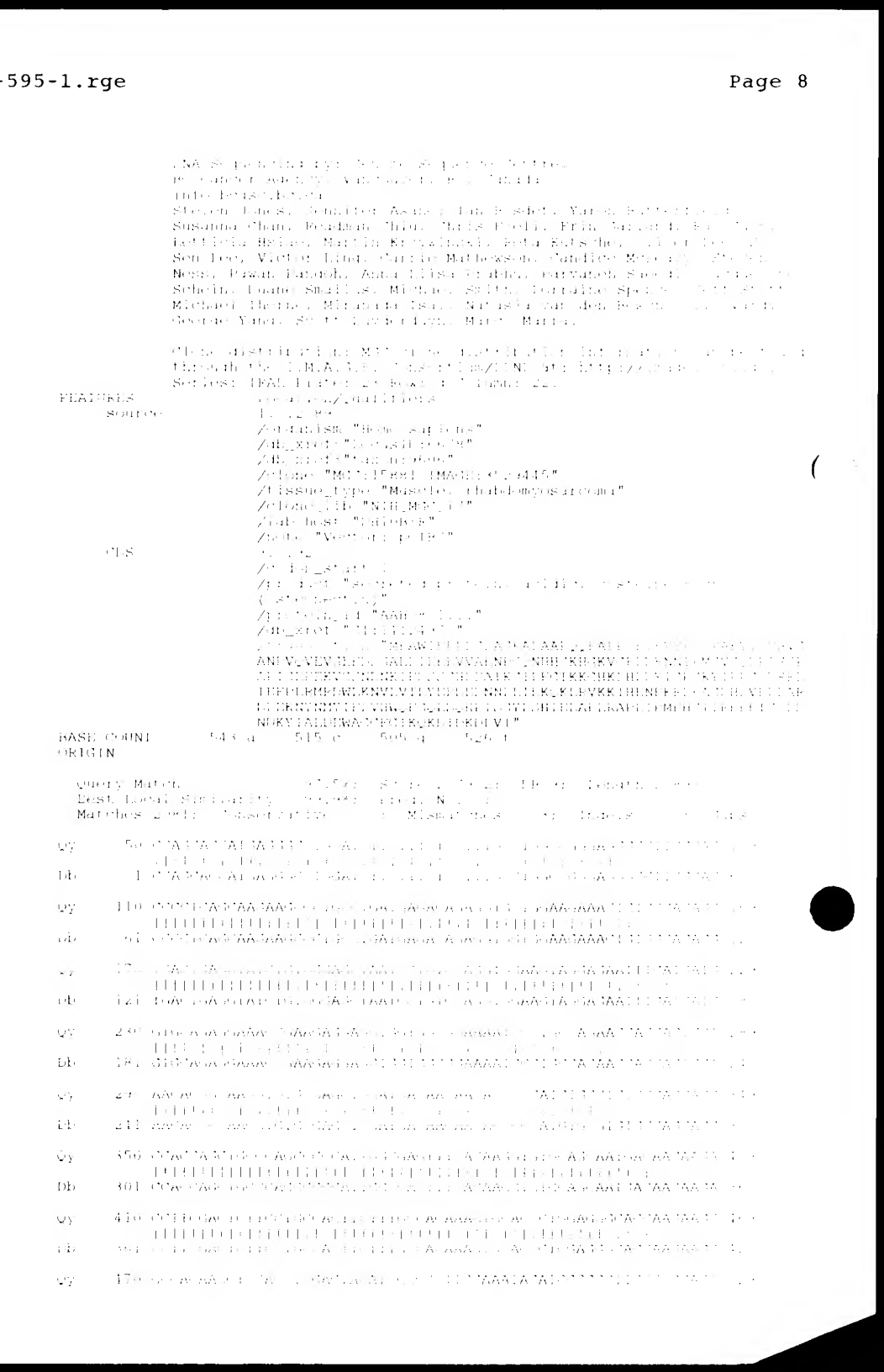
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT





LOCUS BC008011 2089 bp mRNA linear PRI 12-JUL-2002
DEFINITION Homo sapiens, secreted protein, acidic, cysteine-rich (osteonectin), clone MGC:17881 IMAGE:4129415, mRNA, complete cds.
ACCESSION BC008011
VERSION BC008011.1 GI:14124960
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2089)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (17 MAY 2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)



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/lab_host="Stratagene"
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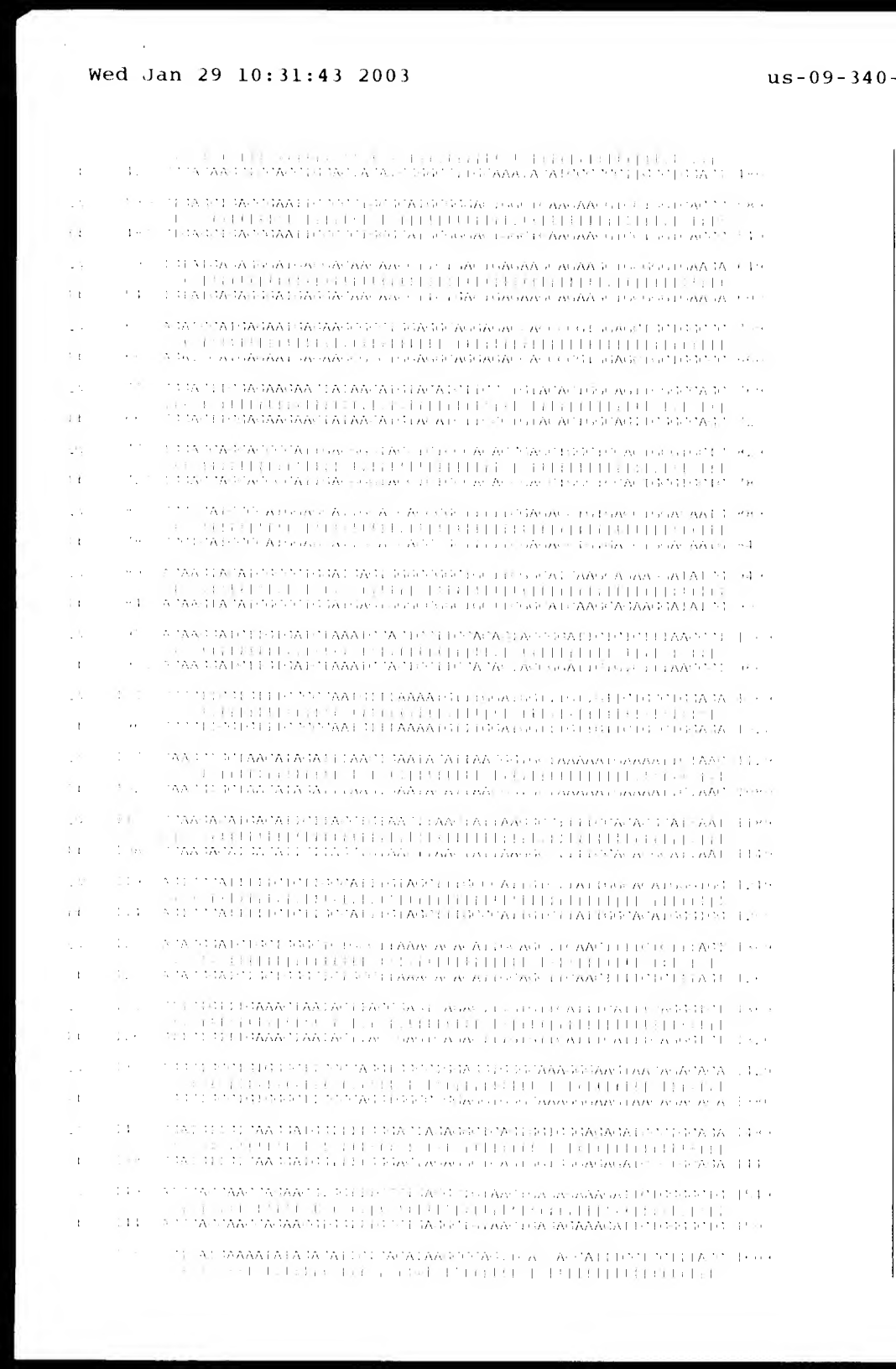
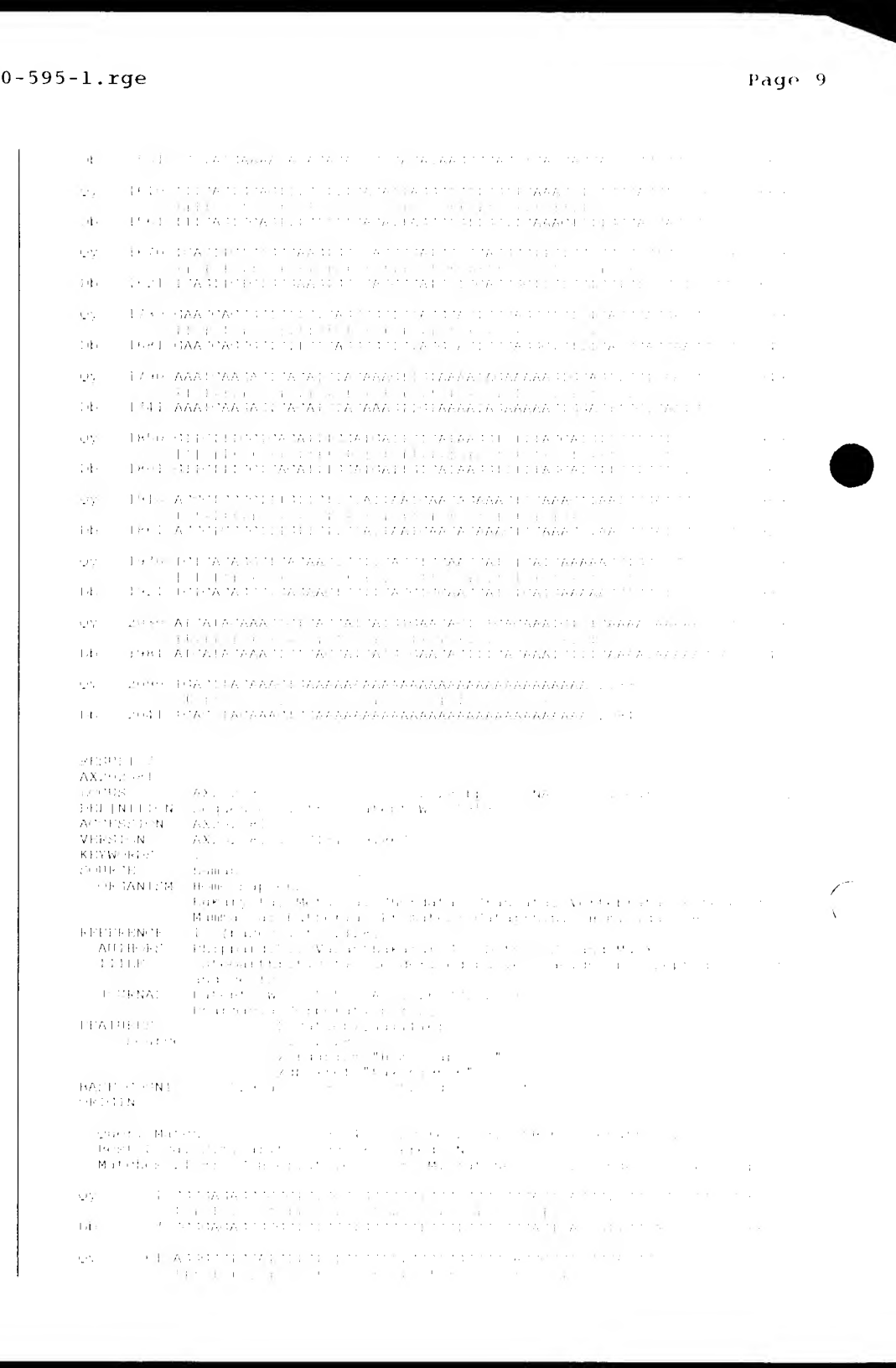
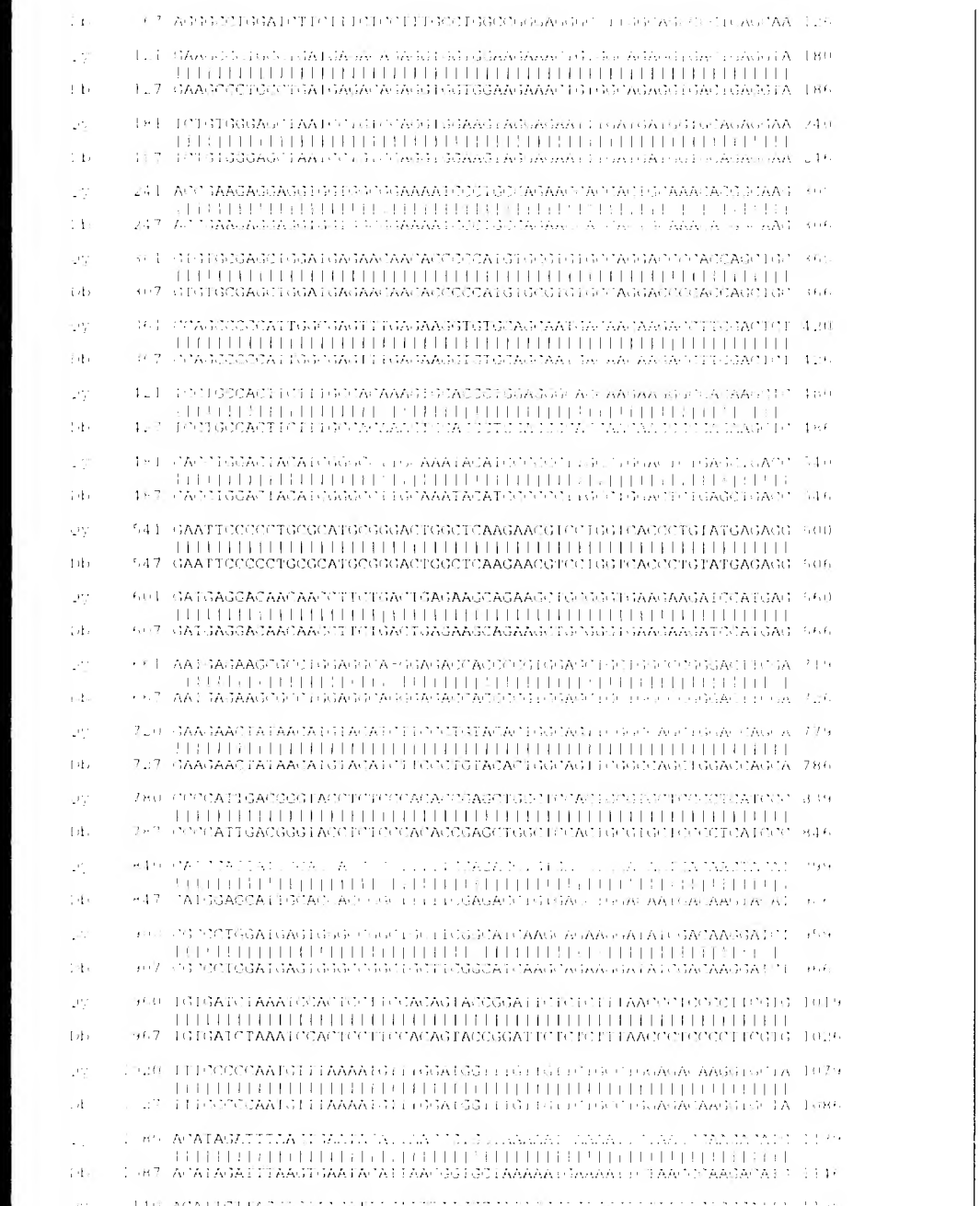
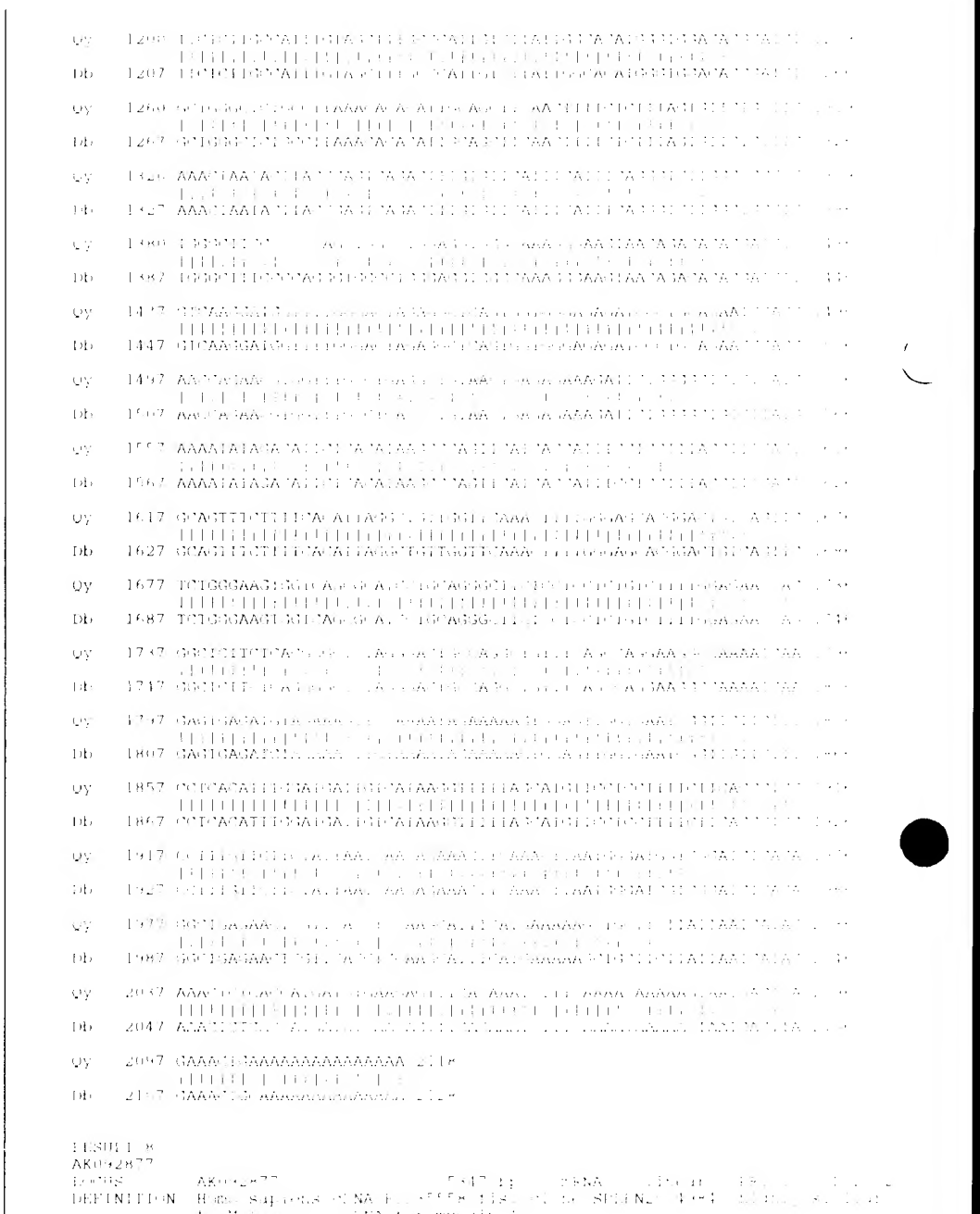
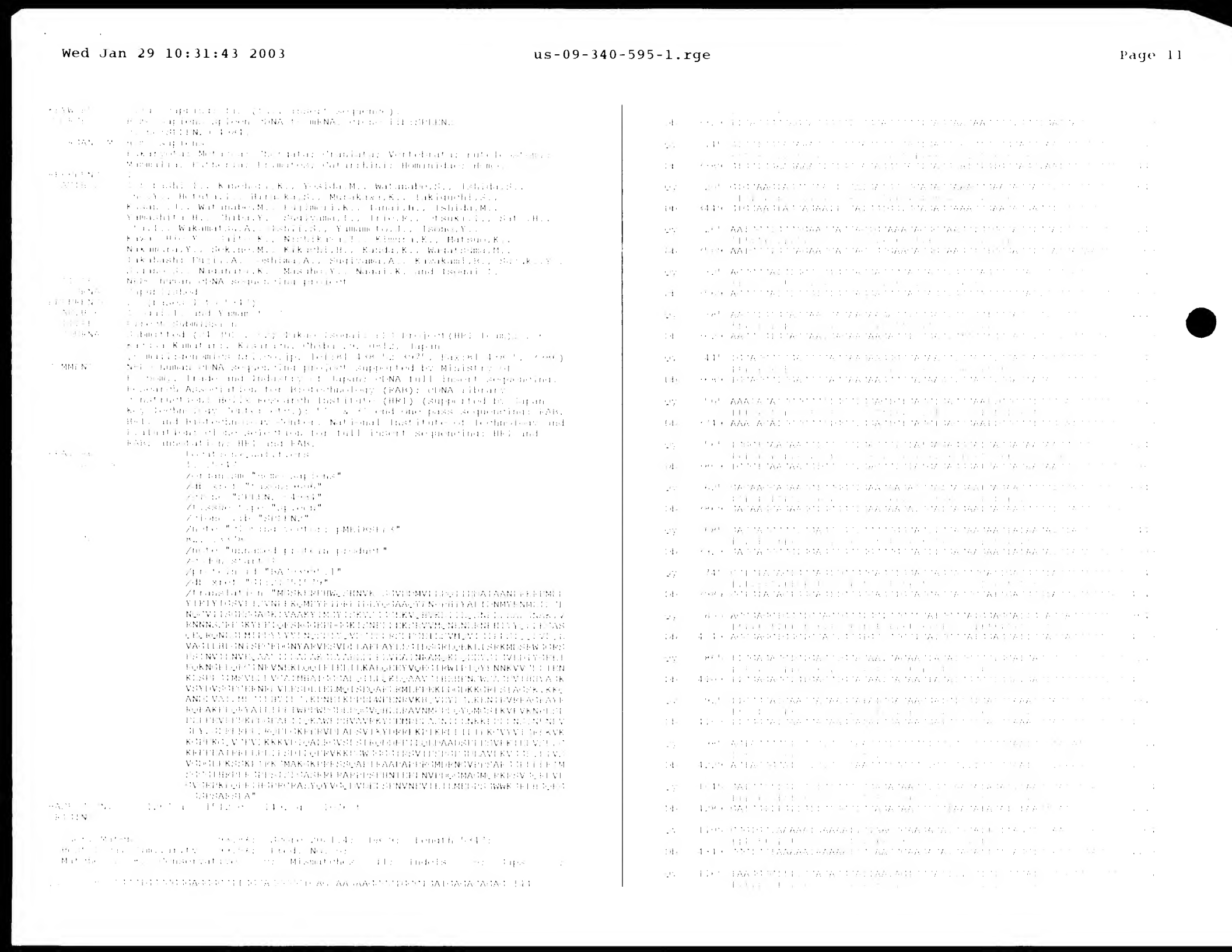
BASE COUNT 543 a 515 c 506 g 526 t
ORIGIN

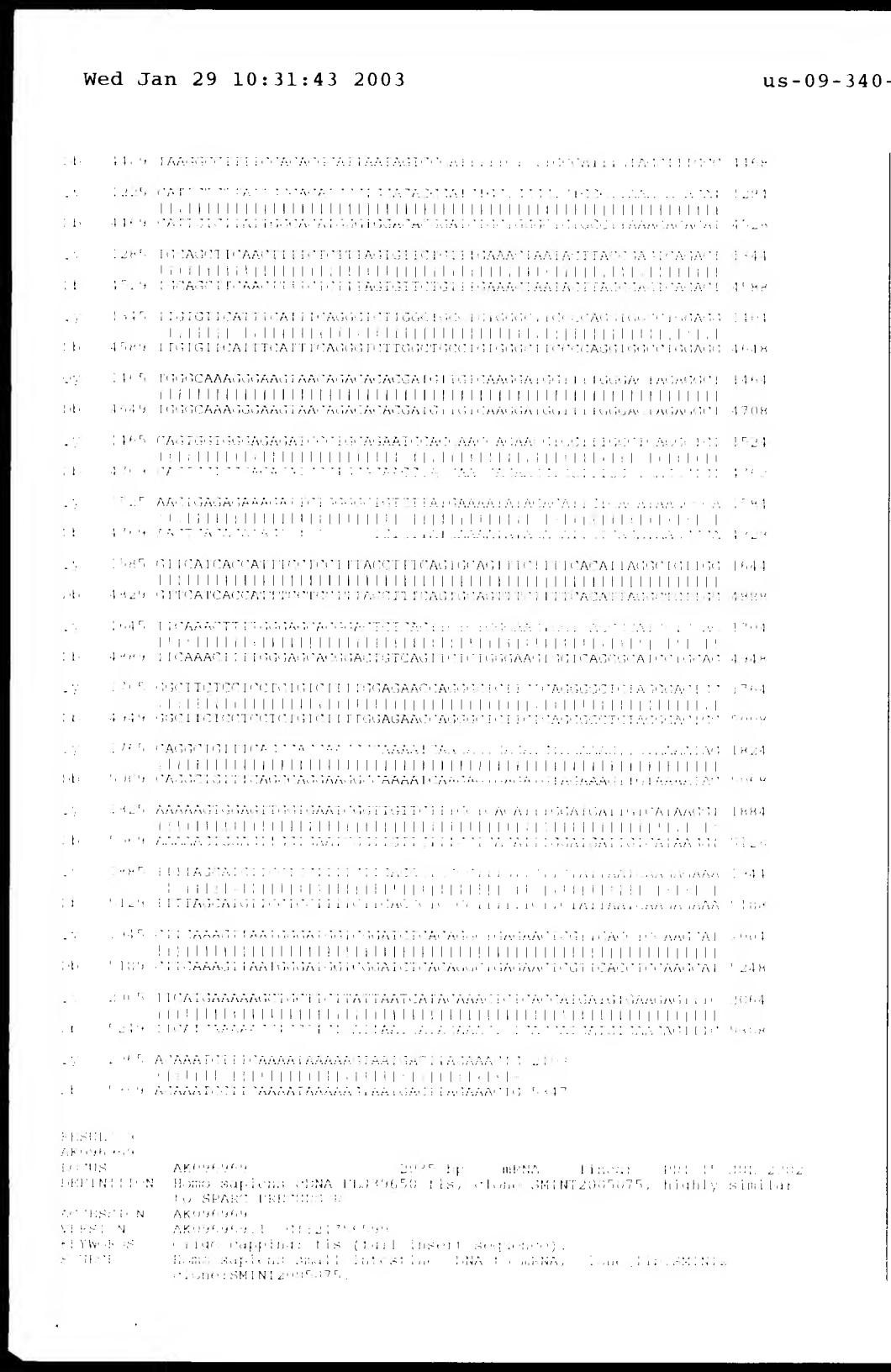












RESULT 1
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LOCUS AK096969 2045 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ39650 fis, clone SMINT2005075, highly similar to SPARC PRECURSOR.
ACCESSION AK096969
VERSION AK096969.1 GI:21757590
KEYWORDS cDNA; Oxppine; fis (full insert sequence).
SOURCE Homo sapiens (small intestine tumor) cDNA clone SMINT2005075.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
REFERENCE 1
AUTHORS [illegible]
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2045)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) [illegible]
(Genetic resources [illegible]
COMMENT NEDO human cDNA sequencing project (Oxppine; fis (full insert sequence).
[illegible]
RAE; annotations: HFI and RAE.
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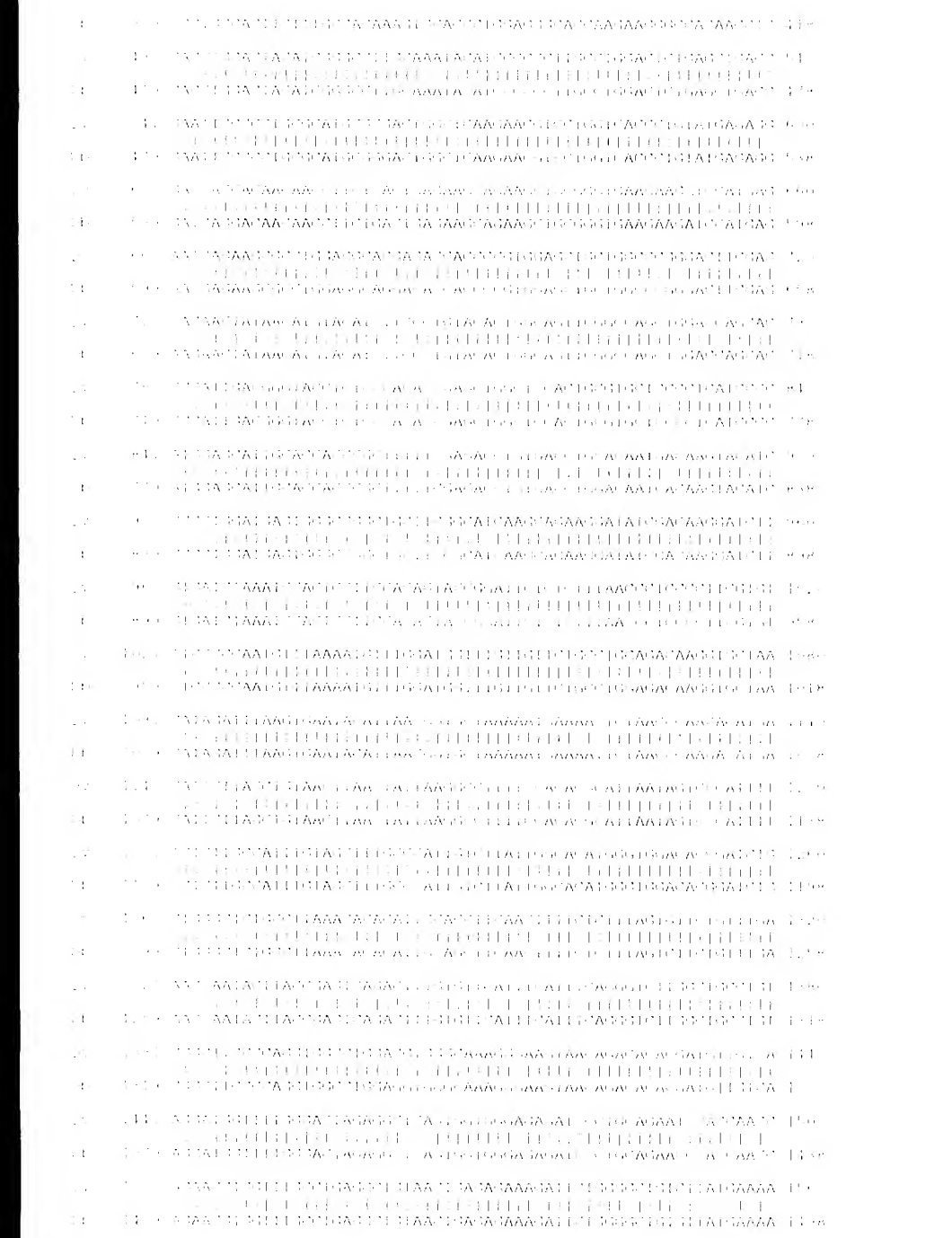
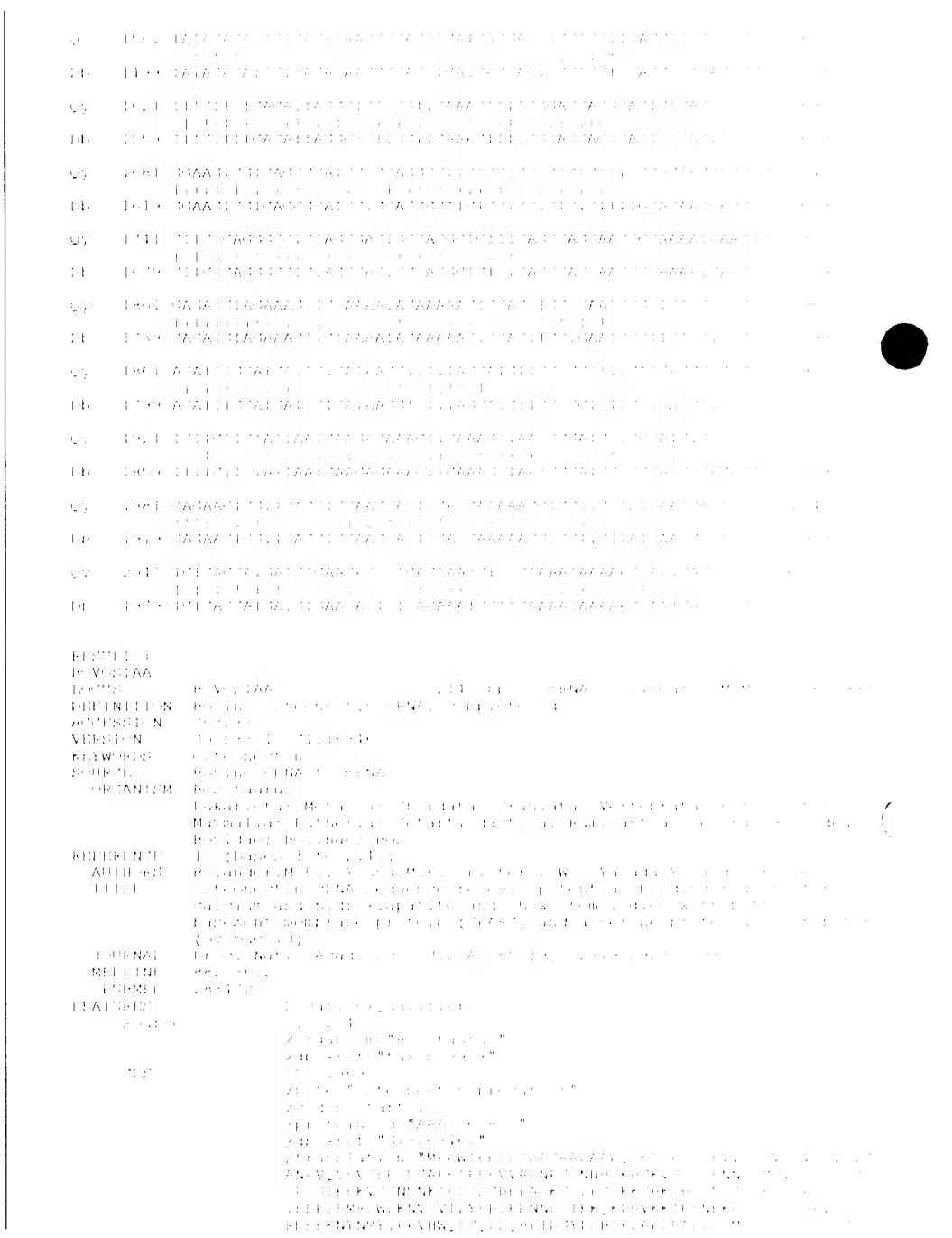
BASE COUNT [illegible]
ORIGIN

Query Match 86.4%; Score 1811; DB 9; Length [illegible]
Best Local Similarity 97.2%; Pred. No. [illegible]
Matches 1965; Conservative 0; Mismatches 47; Indels [illegible]; Gaps [illegible]





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BASE COUNT      523 a    592 c    523 g    585 t
ORIGIN

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Db      13 TGCCTGCTGCCTGCCTGCCTGCCACTGAGGGTTCCCAGCACCATGAGGGCCTGGATCTTC 72

Qy      76 TTTCTCCTTTGCCTGGCCGGGGAGGGCTTGGCAGCCCTCAGCAAGAAGCCTTGCCTGAT 135
           ||||||||||||||||||||||||||||||||||||||||||| || ||||||| |||||||
Db      73 TTTCTCCTTTGCCTGGCCGGGGAGCGCCTTGGCAGCCCCTCAACAGCAAGCCTTGCCTGAT 132

Qy     136 GAGACAGAGGTGGTGGAAGAAACTGTGGCACAGGTGACTGAGGTATCTGTGGGAGCTAAT 195
           ||||||| |||||||||||||| ||||| |||||| | |||||| | |||||||| ||
Db     133 GAGACAGAAGTGGTGGAAGAAACCGTGGCCGAGGTGGCCGAGGTATCCGTGGGAGCCAAC 192

Qy     196 GCTGTCCAGGTGGAAGTAGGAGAATTCGATGATGGTGCTGAGGAAACCGAAGAGATGAGGTG 255
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Qy     256 GTGGCGGAAAATCCCTGCCAGAACCACCACTGCAAACAGGCAAGGTGTGCGAGCTGGAT 315
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Qy     316 GAGAACAACACCGCCATGTGCGTGTGCCAGGACCCCACCAGCTGCCCAGCCGCCATTGGC 375
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Qy     376 GAGTTTGAGAAGGTGTGCAGCAATGACAACAAGAGCTTCGACTCTTCTTGCCACTTCTTT 435
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Qy     436 CCTCTAAATTGCACTTCTTGAGTCCTCTCAAGAAGCTGCGCAAGTCTTACTCTGAGTTATC 495
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Qy     496 GGGCCTTGCAAATACATCCCCCCTTGCCTGGACTCTGAGCTGACCGAATTCCCCCTGCGC 555
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Qy     556 ATGTCGGGACTGGCTTCAAGAACCTCCTTGATCACCTCGTATCAGAGAGCATCAGCACAACAC 615
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Qy     616 CTTCTGAATTGAAAATTAAAAATTCCTTTTTGAAAAAAGTTGATGAAAATGAAAGCGCCTG 675
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Qy     676 GAGGCAG   GAGACGACCCCGTGGAGCTGCTGGCCCGGGACTTCGACAAGAACTATAAC 732
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Qy     733 ATGTACATCTTCGCCTGTACACTGGCAGTTCGGGCAGCTGGATGAGCACCGCATTGACGGG 792
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Qy     853 ATCGCCGCCTTTTTCGAGGCCTTCTGGCCCGACGTGCAATCCGACTTCGTCCTCCACGAG 912
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Db     853 ACCGACGGCTTTTTCGAGACATGTGACCTGGACAACGACAAGTACATCGCCTTGGACGAG 912

Qy     913 TGGGCCGGCTGCTTCGGCATCAAGCAGAAGATATCCACAAGGATCTTCGAGTCTAAAATC 972
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Db     973 GAGCTCCTTCCATACTACGGATTCTCTCTTAACCTTCCCTTCCTCCTCCCCTCCCC 1032

Qy    1029 ACCCCCCCAAA.....AA.CC.....C.....C.....CAAATATAAA  1080
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Qy    1081 CTAA.AAAAAAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1140
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Qy    1201 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1260
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Qy    1261 CTCCGCCTTAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1320
           || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1273 CTCCGCCTTAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1332

Qy    1321 ATAATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1380
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Db    1333 ATAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1392

Qy    1381 TTCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1440
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Qy    1791 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1850
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Qy    1893 --CCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1950
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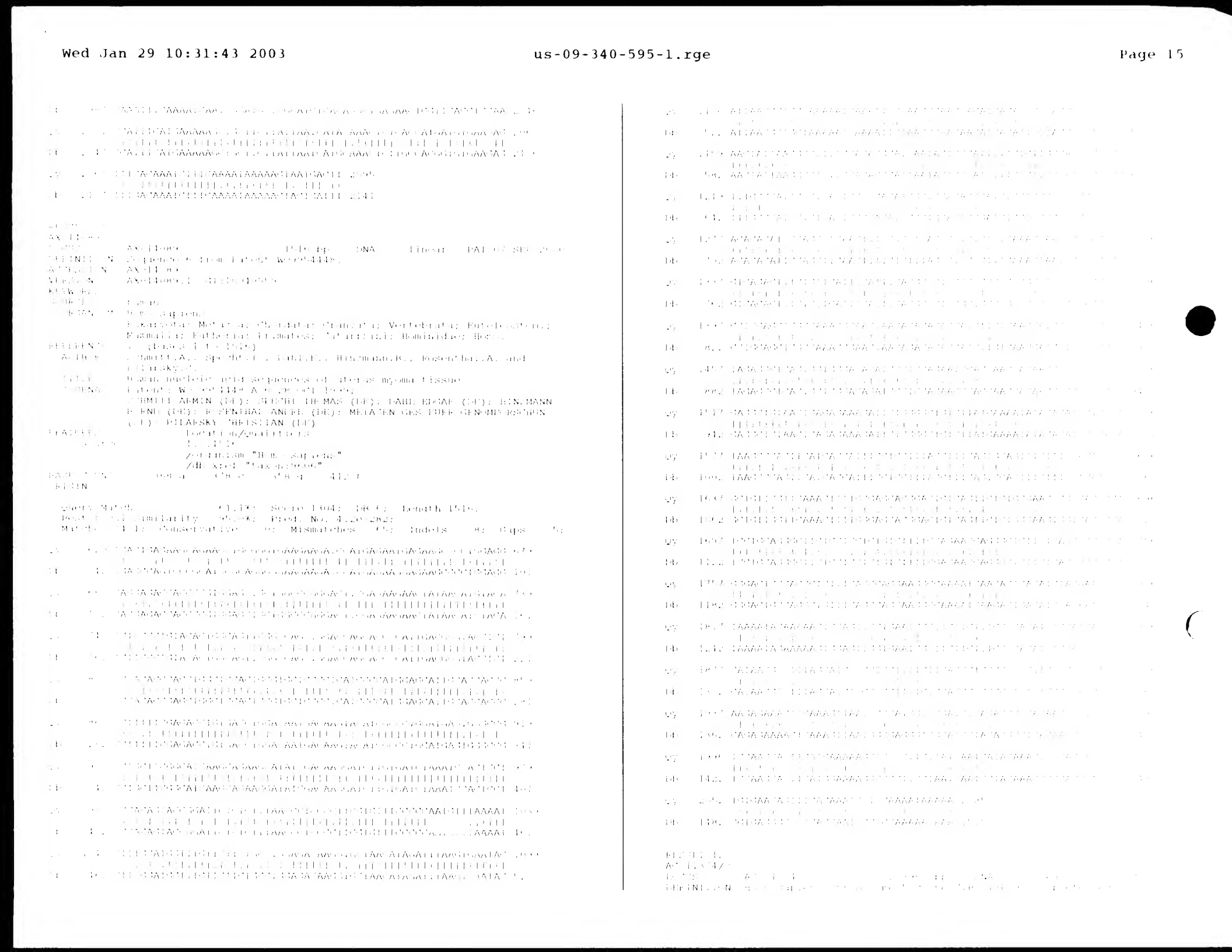

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VERSION     AC011374.6  GI:19747126
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SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 203961)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-OCT-1999) DOE Joint Genome Institute, 2800 Mitchell
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   2  (bases 1 to 203961)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:14752662.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
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BASE COUNT    55939 a   46473 c   46957 g   54592 t
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  Query Match             54.2%;  Score 1156.6;  DB 9;  Length 203961;
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  Matches 1159;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db  112340 AAGATATCGACAAGGATCTTGTGAGTTAAATGCACTGCTTGCACAGTTACCGGATTCTCTC 112281

Qy    1001 TTTAACCCTCCCCTTCGTGTTTCCCCCAATGTTTAAAATGTTTGGATGGTTTGTTGTCT 1060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  112280 TTTAACCCTCCCCTTCGTGTTTCCCCCAATGTTTAAAATGTTTGGATGGTTTGTTGTCT 112221

Qy    1061 GCCTGGAGACAAGGTGCTAACATAGATTTAAGTGAATACATTAAGGGCCTAAAAATGAA 1120
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Db  112220 CGCTGGAGACAAGGTGCTAACATAGATTTAAGTGAATACATTAAGGGCCTAAAAATGAA 112161

Qy    1121 AATCTTAATCCAAACATAGACTTTAGCTGTAACTTAACTATTAAGCCTTTTGCAA 1180
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Qy    1181 CGCATTAATAGTCCCATTTTTCTCTTGCCATTTGTAGCTTTGCCCATTGCTTATTGGCA 1240
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Qy    1241 GATTCTGAAGAGCTATGTCCTAAAGCTATTTTGATTTAATTTCT 1283
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Qy    1344 TCAGGGTCTTGGCTGCCTGTGGGCTTCGCCAGGTGGCTCGAGGTGGGTAAAGGAAATA 1403
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VERSION     AX188083.1  GI:15129555
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE   1  (bases 1 to 4778)
  AUTHORS   [illegible] and Zhang,X.
  TITLE     Genes, compositions, kits, and methods for identification,
            assessment, prevention, and therapy of cervical cancer
  JOURNAL   Patent: WO 0142167-A 4778 14-JUN-2001;
            Millennium Predictive Medicine, Inc. (US)
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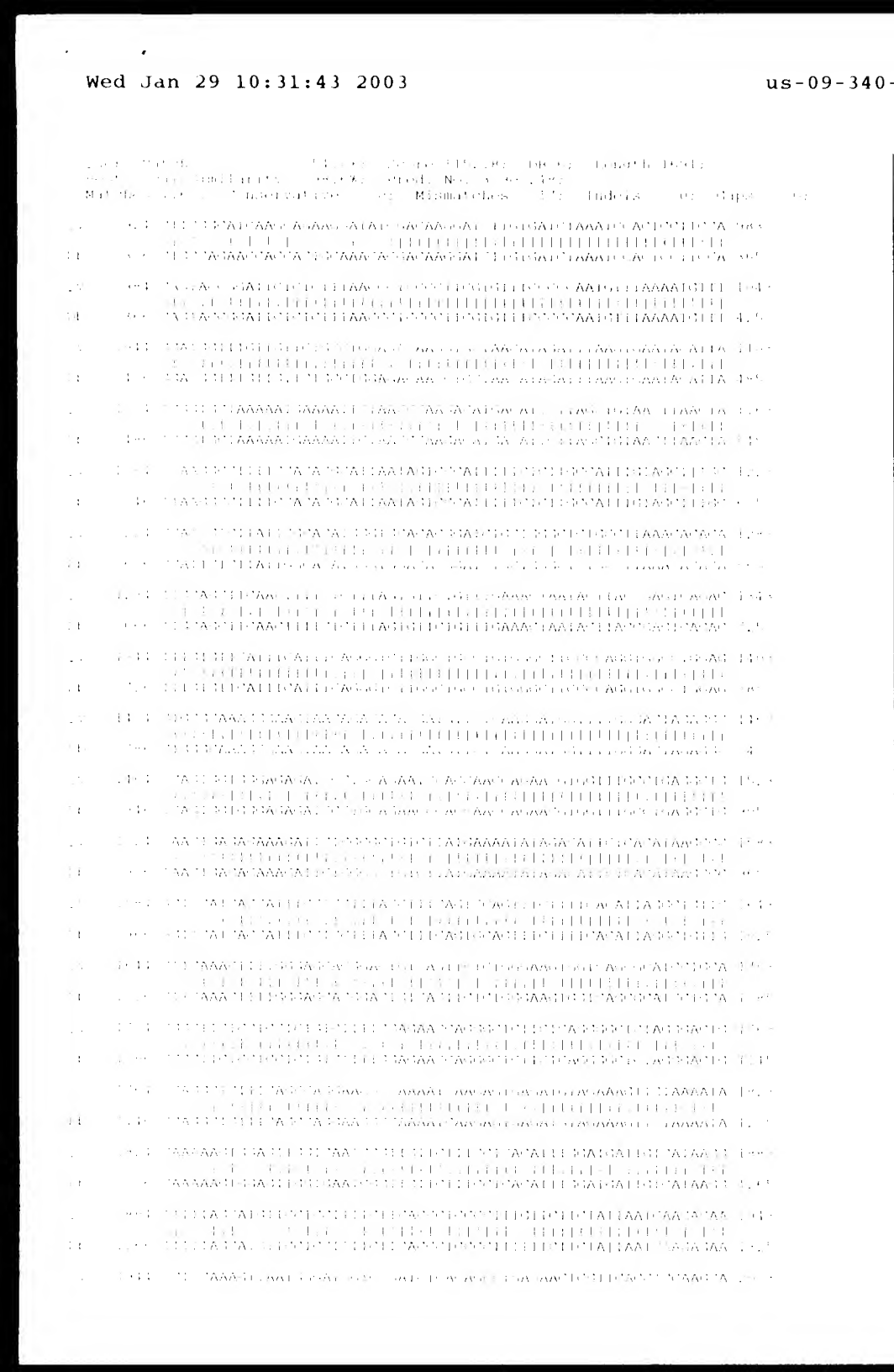

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Qy       1121 AATTCTAACCCAAGACATGACATTCTTAGGTGTAACTTAACTATTAA[illegible] 1180
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Qy       2021 [illegible]
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RESULT 15
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DEFINITION  Sequence 1 from patent US 6239326.
ACCESSION   AR156028
VERSION     AR156028.1  GI:15124081
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2079)
  AUTHORS   Howe,C.P.
  TITLE     Sparc-deficient transgenic mice
  JOURNAL   Patent: US 6239326-A 1 29-MAY-2001;
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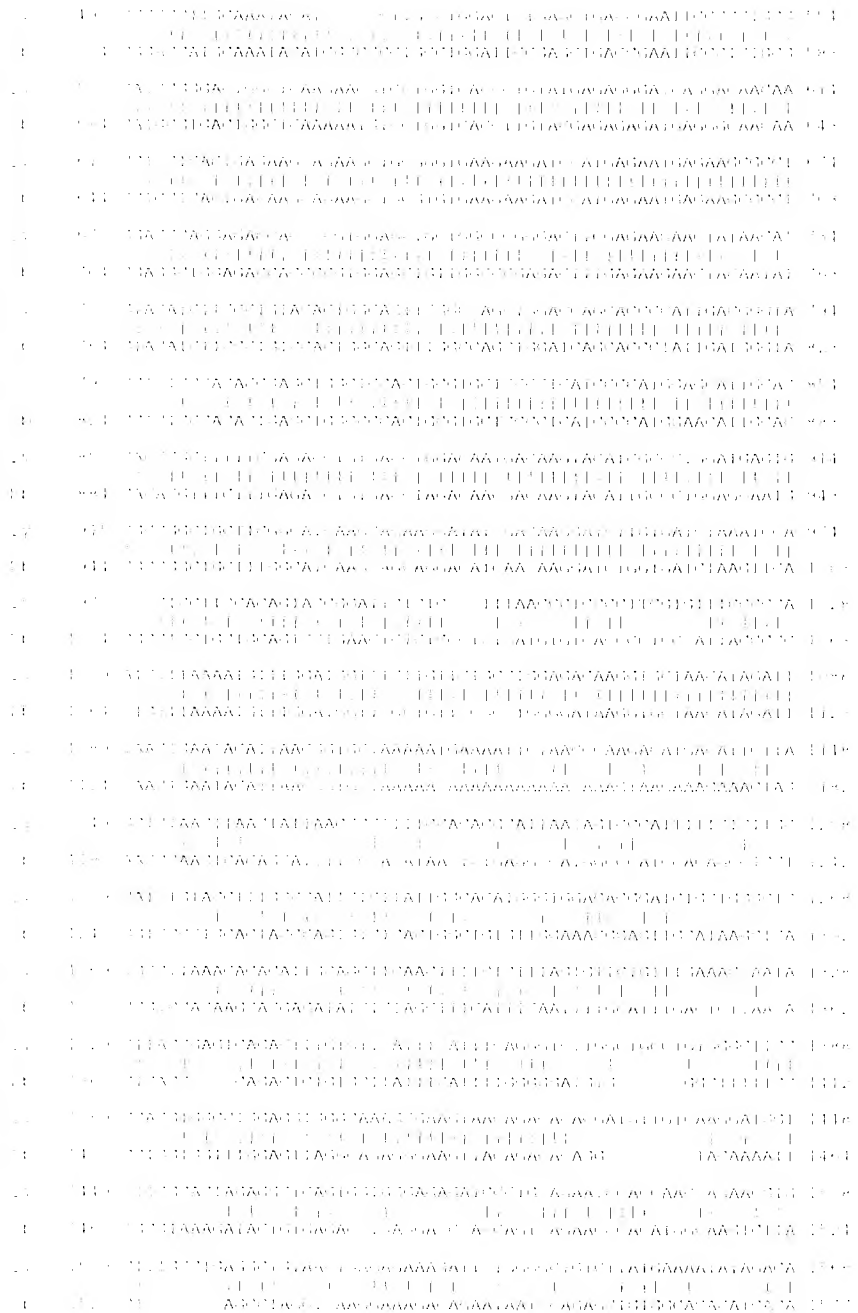
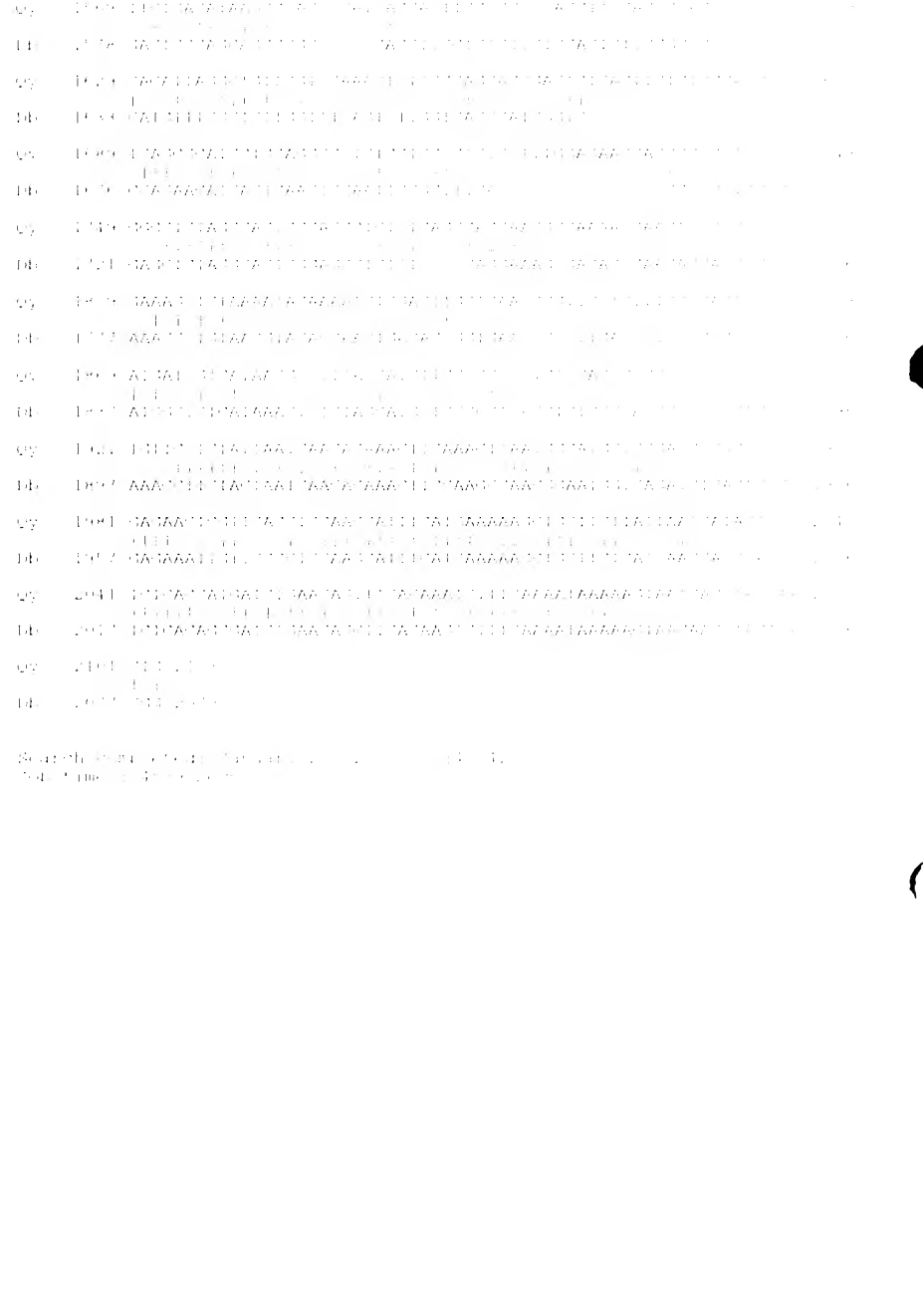
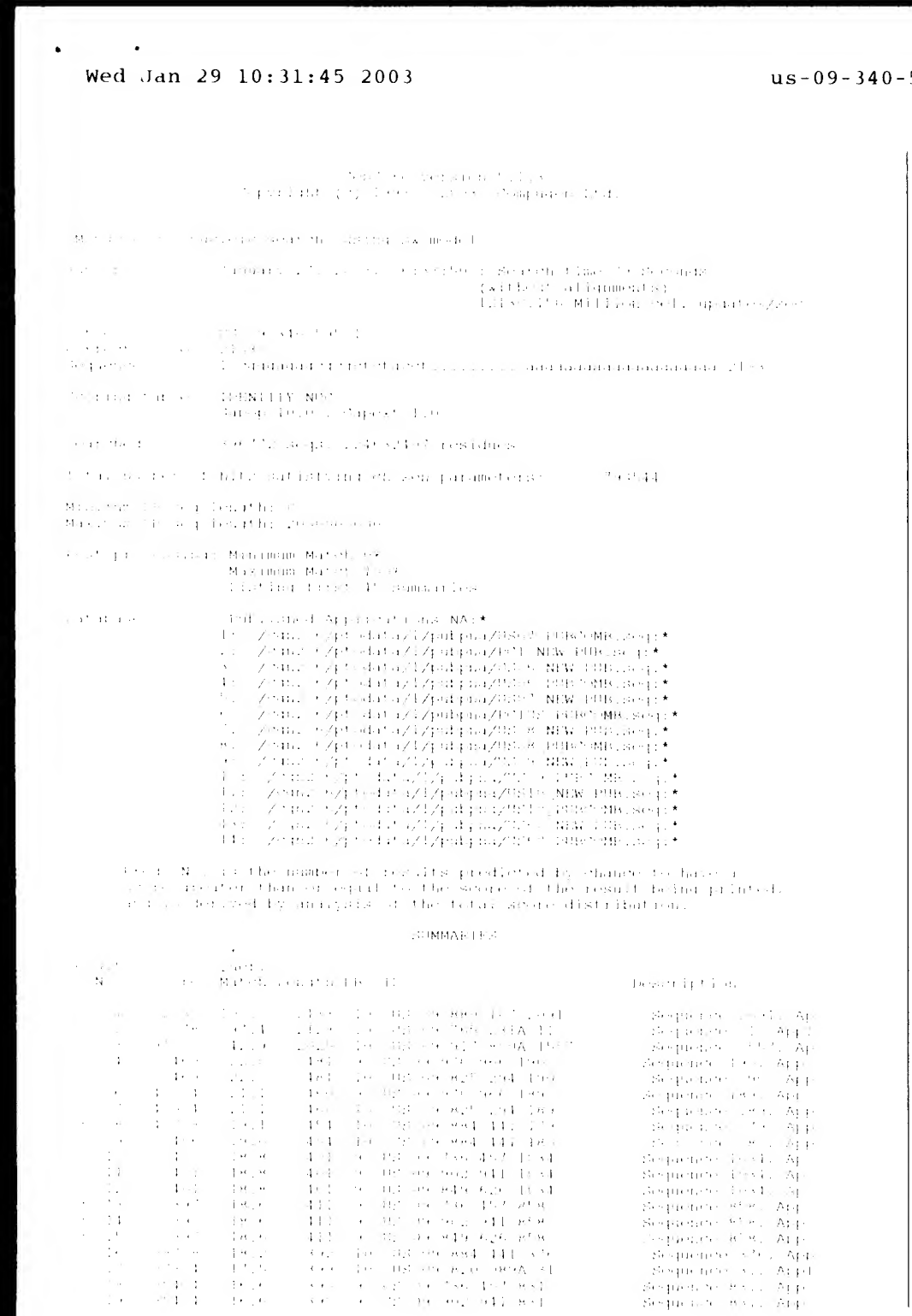
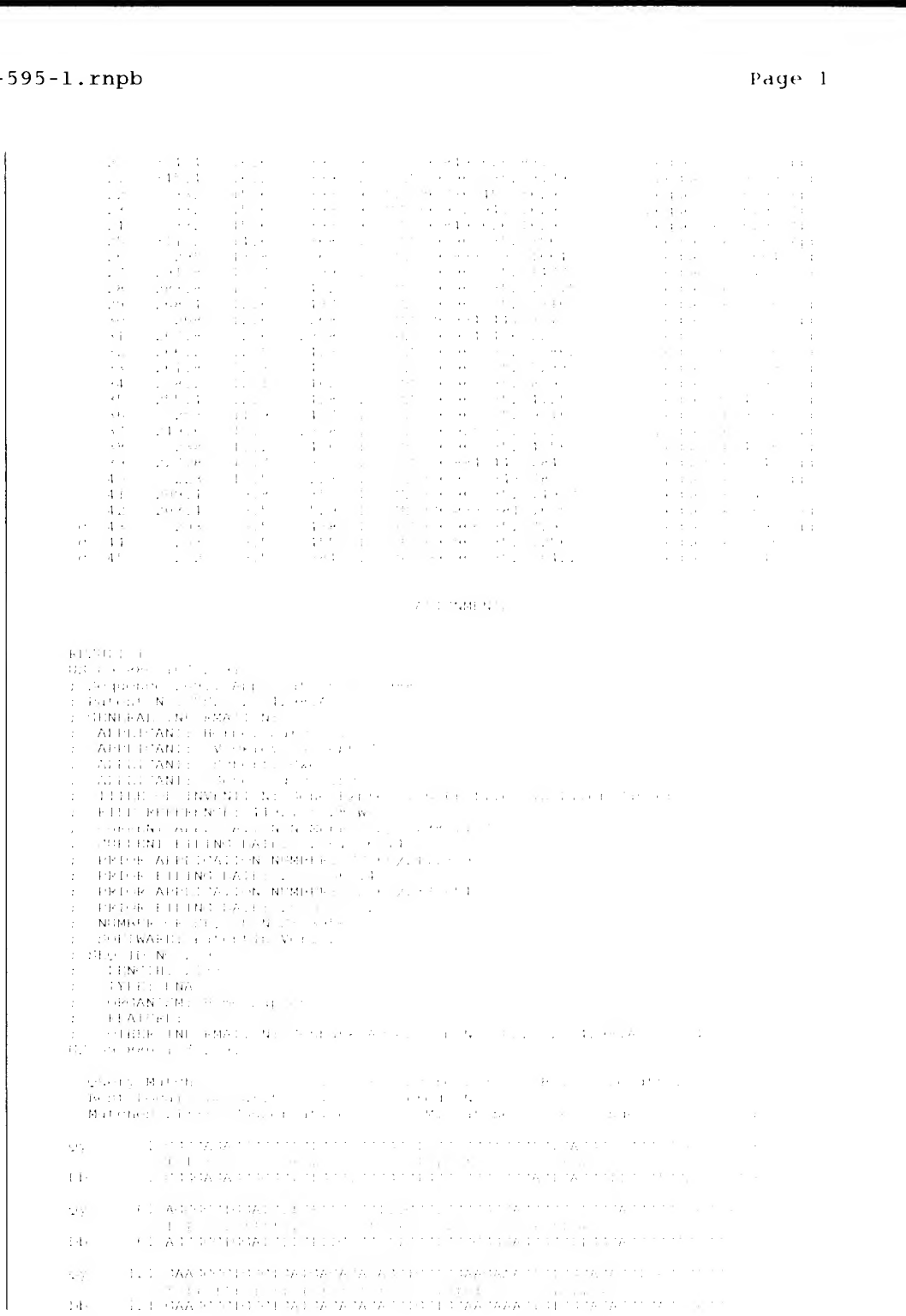
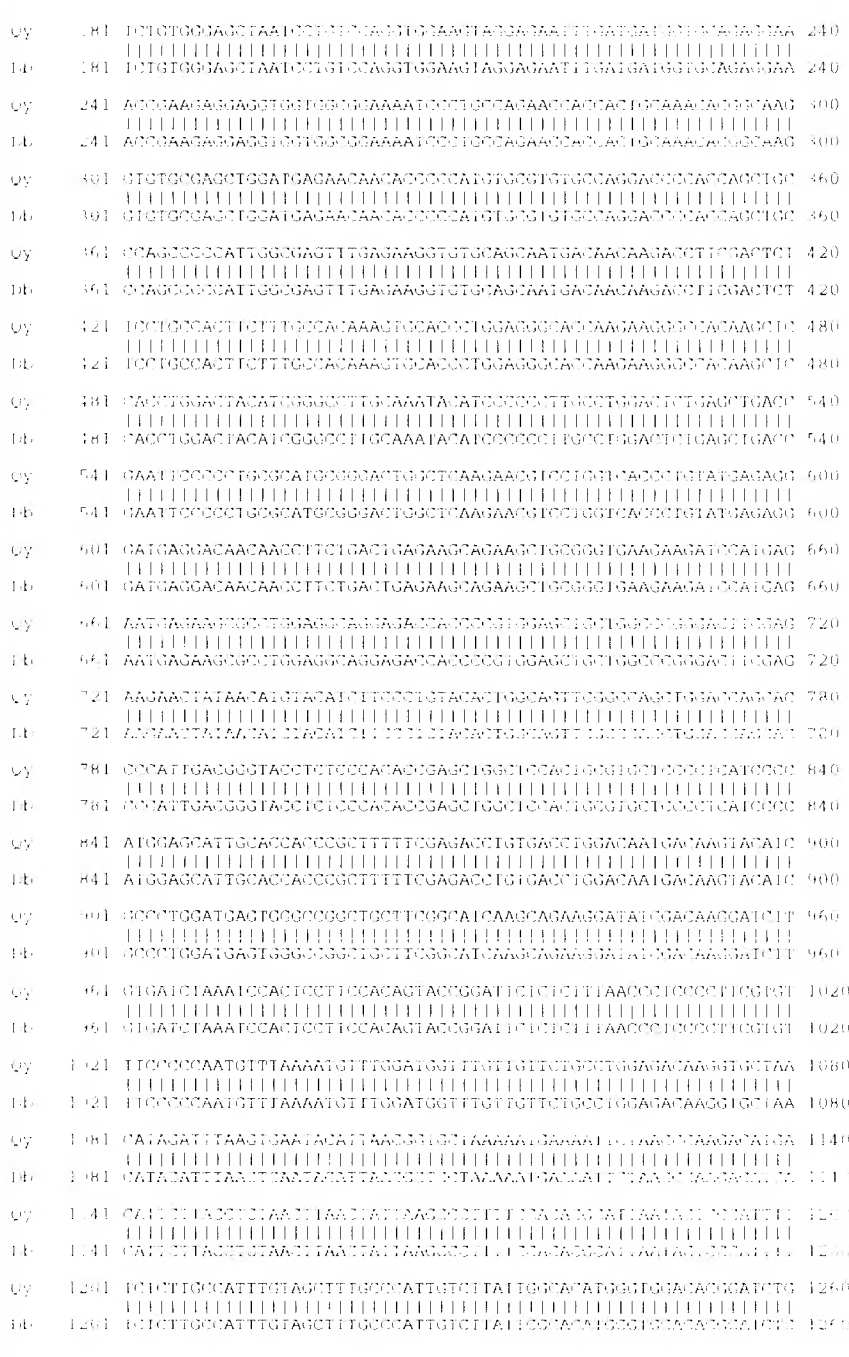
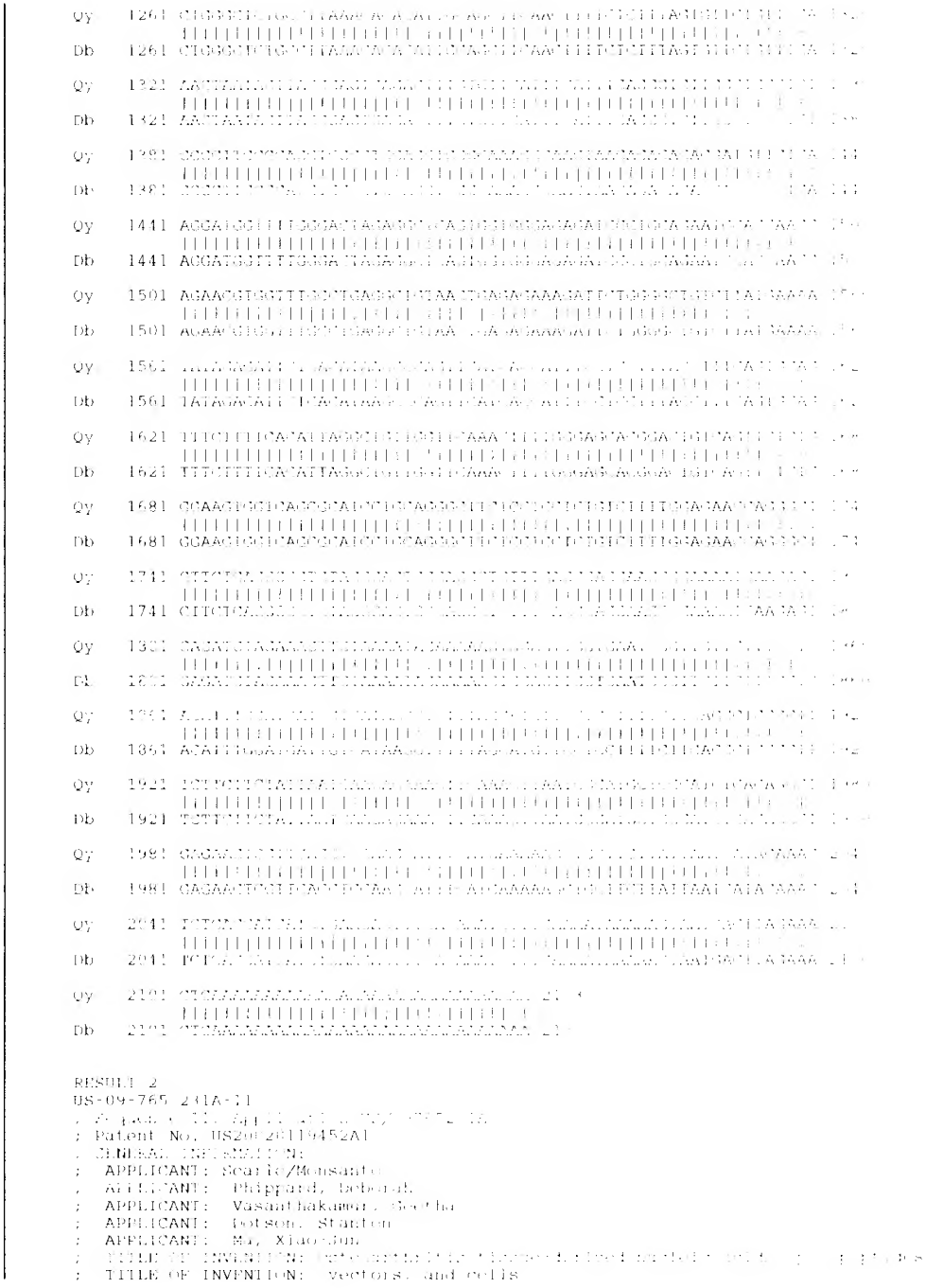




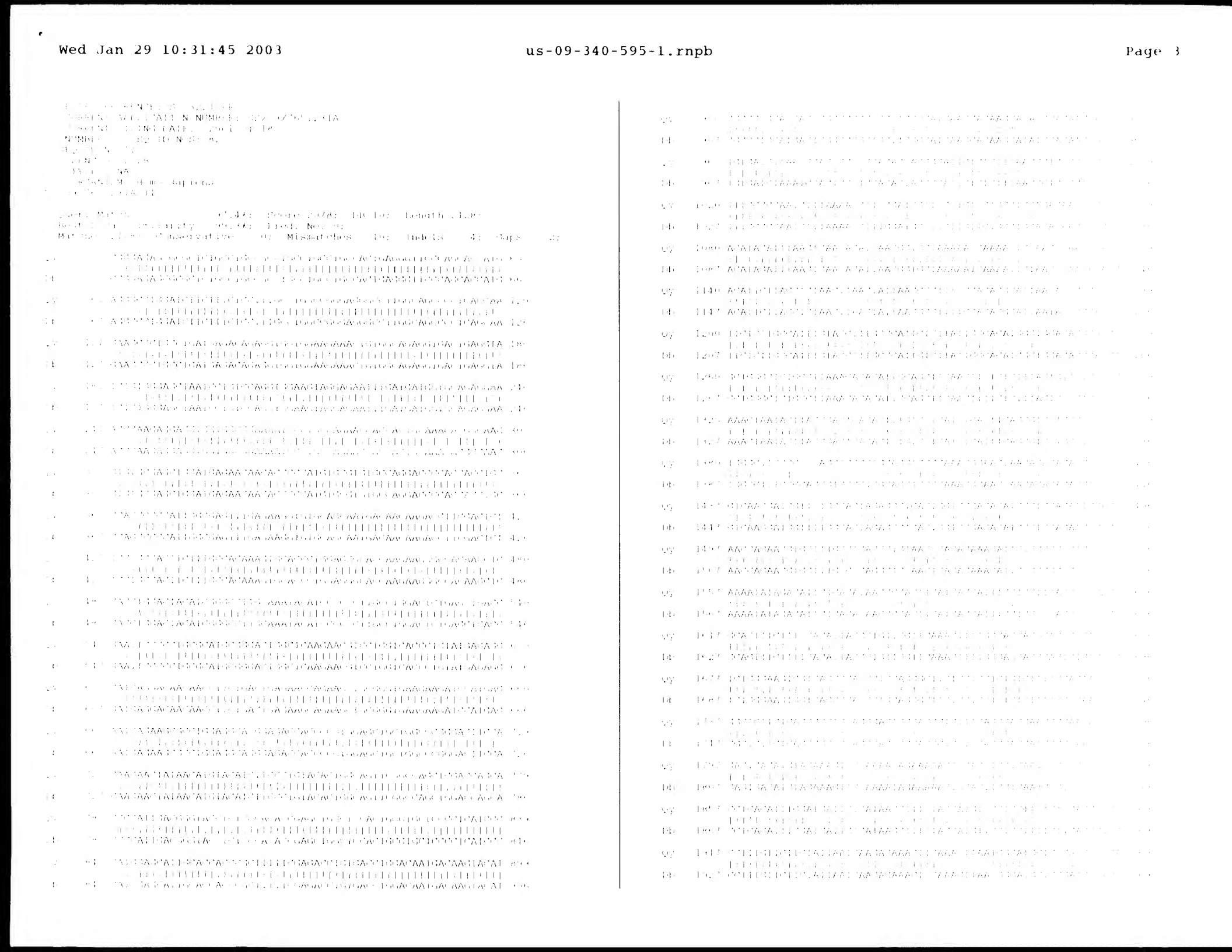


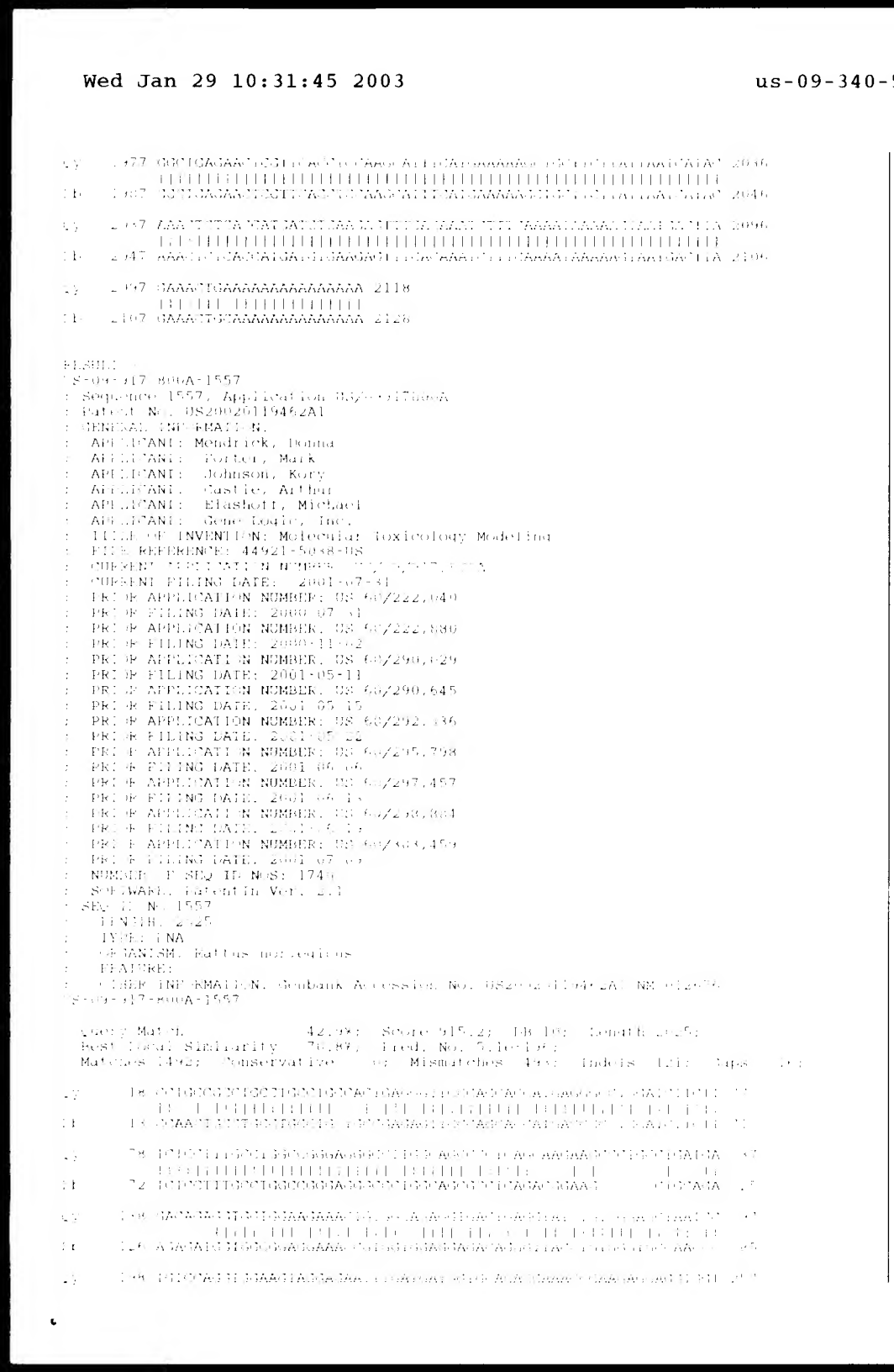






RESULT 2
US-09-765 281A-11
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Scarlo/Monsanto
; APPLICANT: Philpard, Deborah
; APPLICANT: Vasanthakumar, Sudha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiaojun
; TITLE OF INVENTION: [illegible]
; TITLE OF INVENTION: Vectors and cells





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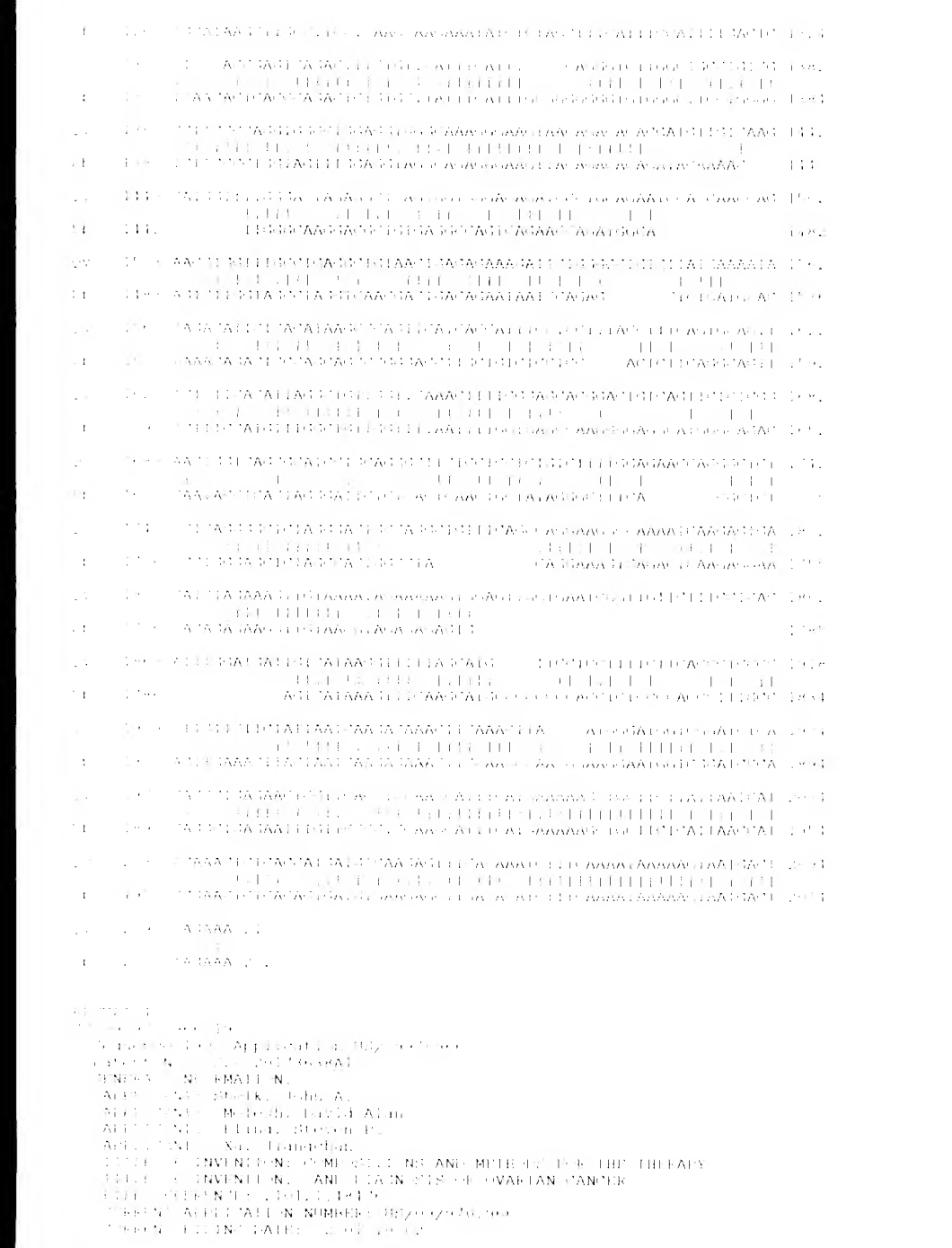
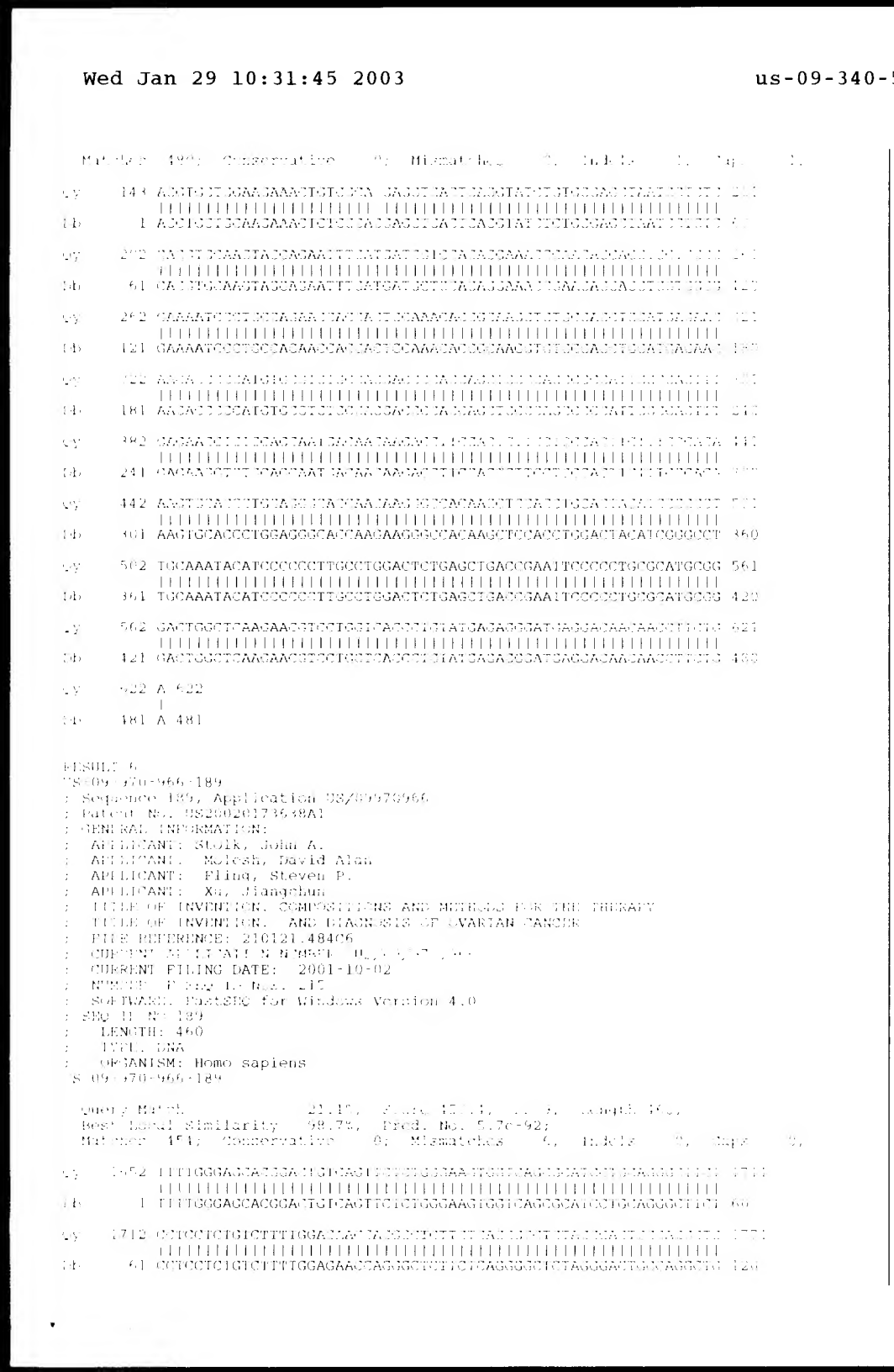
ORIGIN





RESULT 6
US-09-970-966-189
; Sequence 189, Application US/09970966
; Patent No. US20020173648A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: McIeah, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.48406
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 189
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-189

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Matches 454; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 7
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; Sequence 189, Application US/09825294
; Patent No. US20020091491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.48405
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 189
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-189

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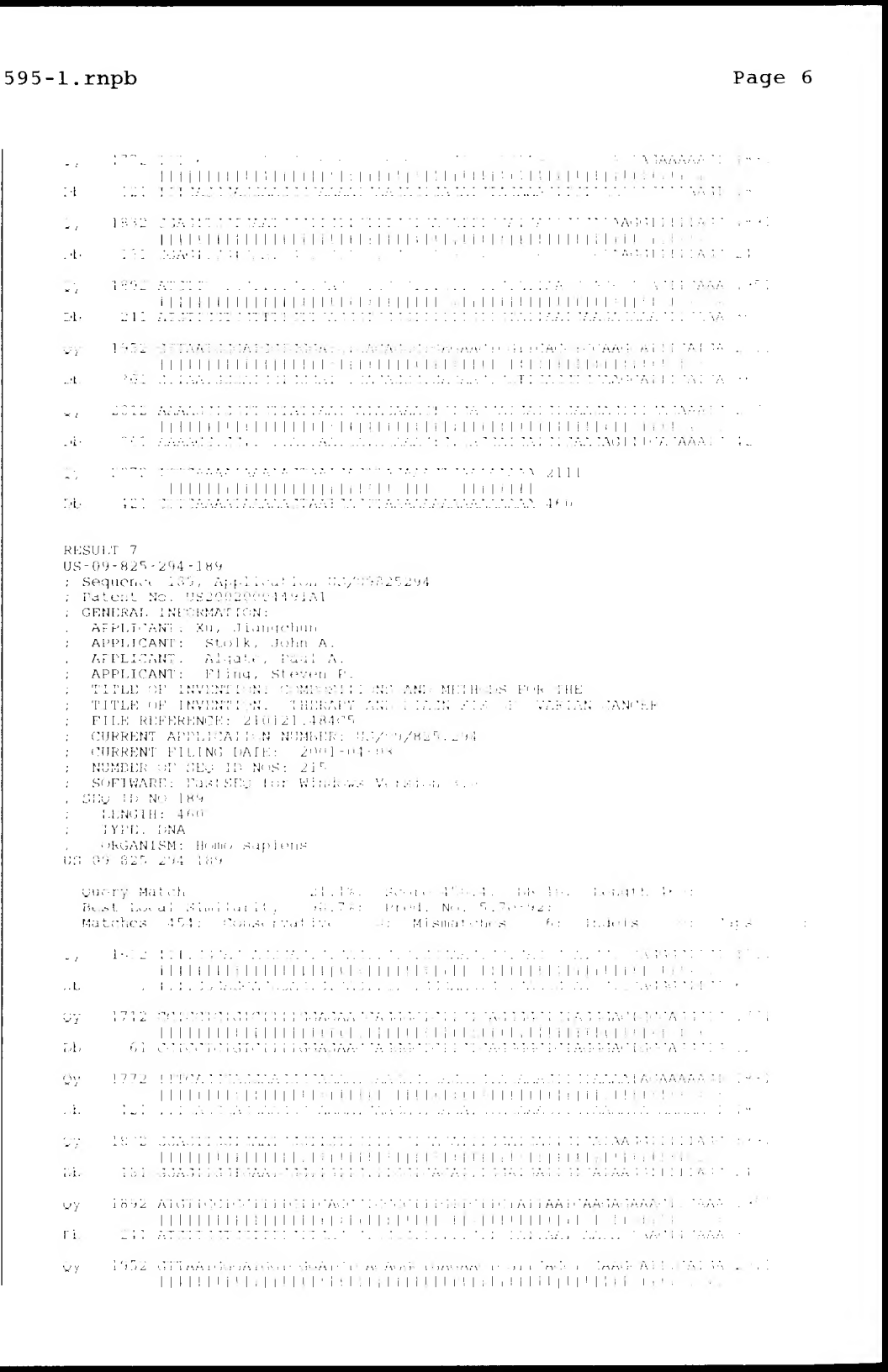
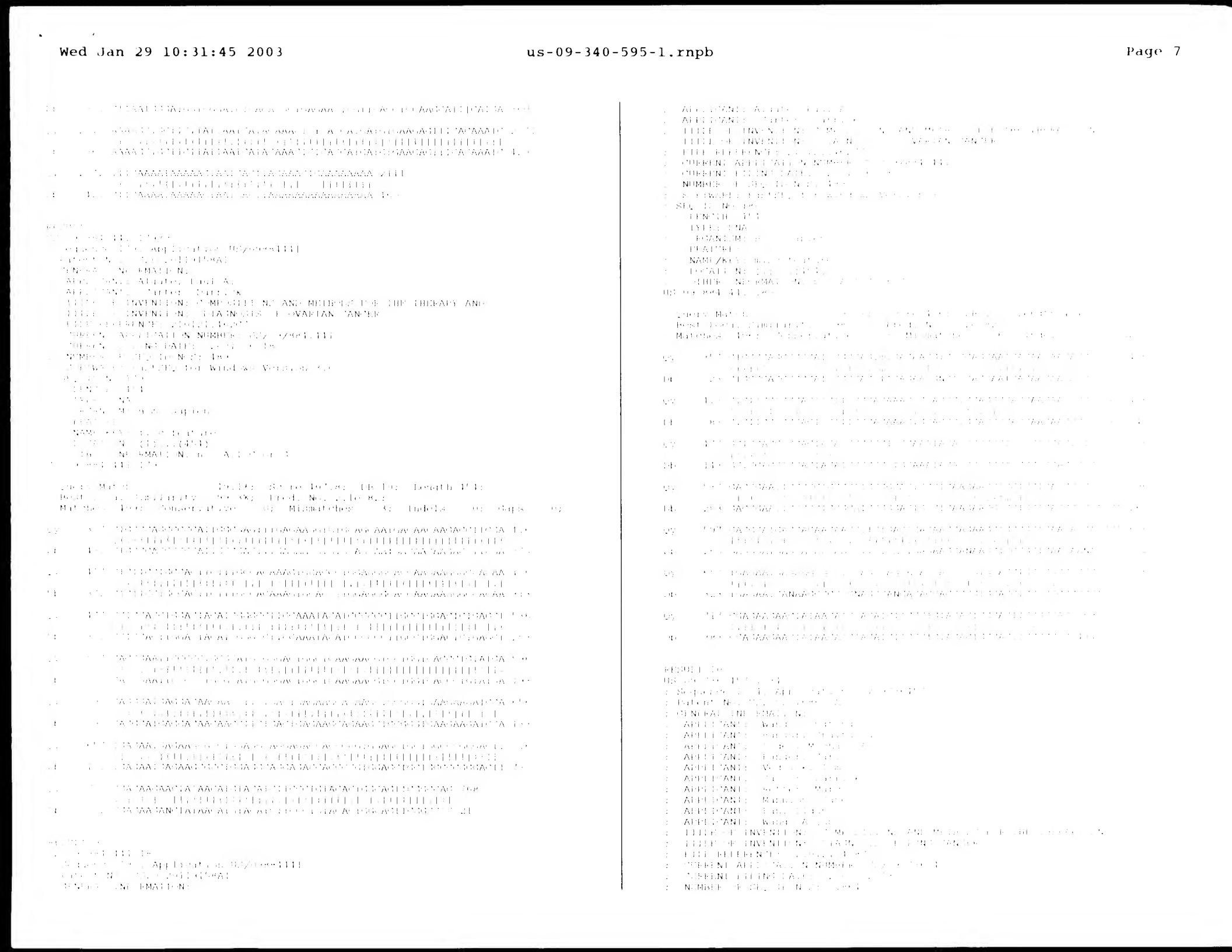
Best Local Similarity 98.7%; Pred. No. 5.7e-92;
Matches 454; Conservative 0; Mismatches 6; Indels 0; Gaps 0;





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; SEQ ID NO 1034
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-736-457-1034

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  Matches  401;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     829 CCCCTCATCCCCATGGAGCATTGCACCACACCGCTTTTTCGAGACCTGTGACTCTGGACAAT 888
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RESULT 11
US-09-902-941-1034
; Sequence 1034, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT: Wang, Tongtong
;  APPLICANT: Watanabe, Yoshihiro
;  APPLICANT: Johnson, Jeffrey C.
;  APPLICANT: Retter, Marc W.
;  APPLICANT: Marnerakis, Margarita
;  APPLICANT: Carter, Darrick
;  APPLICANT: Fanger, Gary R.
;  APPLICANT: Vodvick, Thomas S.
;  APPLICANT: Bangur, Chaitanya S.
;  APPLICANT: McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 21012/478912
;  CURRENT APPLICATION NUMBER: US/09/902,941
;  CURRENT FILING DATE:  2001-07-10
;  NUMBER OF SEQ ID NOS: 2002
;  SOFTWARE: PatentSEQ for Windows Version 1.0
; SEQ ID NO 1034
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-902-941-1034

  Query Match             18.8%;  Score 401;  DB 9;  Length 401;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-21;
  Matches  401;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     769 CTGGACCAGCAGCCCCATTGACGGGTACCTCTCCCACACCGAGCTGGCTCCACTGCGTGCT 828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGGACCAGCAGCCCCATTGACGGGTACCTCTCCCACACCGAGCTGGCTCCACTGCGTGCT 60

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     889 GACAAGTACATCGGCCCTGGATGAGTGGGCCGGCTGCTTCGGCATCAAGCAGAAGGATATC 948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     949 GACAAGGATCTTGTGATCTAAATCCACTCCTCCACAGTACCGGATTCTCTCTTTAACCC 1008
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; Sequence 1, Application US/09849626
; Publication No. US20020137058A1
; GENERAL INFORMATION:
;  APPLICANT: Bangur, Chaitanya
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Switzer, Anne
;  APPLICANT:  McNeill, Patricia
;  APPLICANT:  Clapper, Jonathan
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AN
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 21012/478912
;  CURRENT APPLICATION NUMBER: US/09/849,626
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 1926
;  SOFTWARE: PatentSEQ for Windows Version 1.0
; SEQ ID NO 1034
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-849-626-1034

  Query Match             18.8%;  Score 401;  DB 9;  Length 401;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-21;
  Matches  401;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     769 CTGGACCAGCAGCCCCATTGACGGGTACCTCTCCCACACCGAGCTGGCTCCACTGCGTGCT 828
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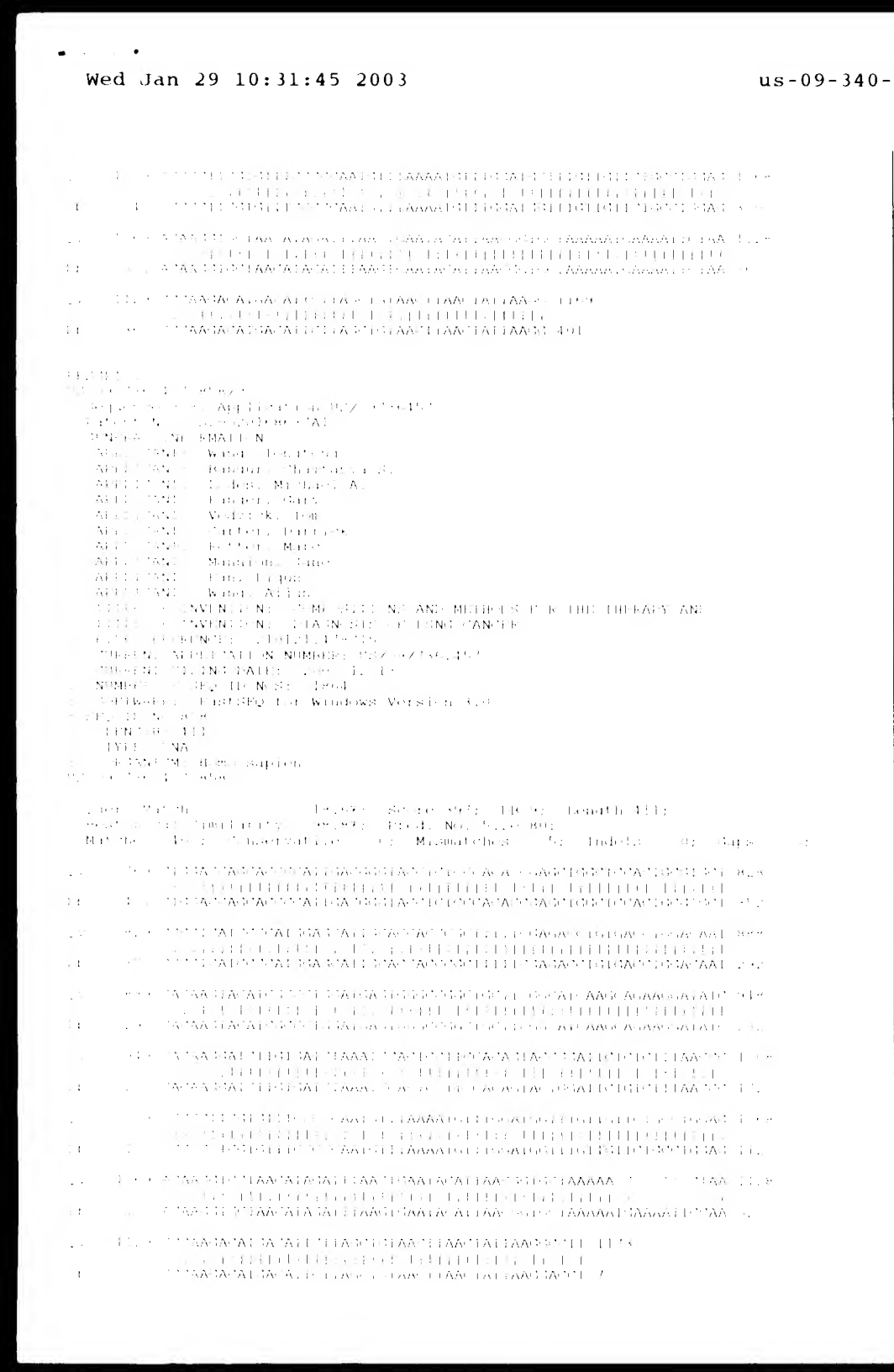

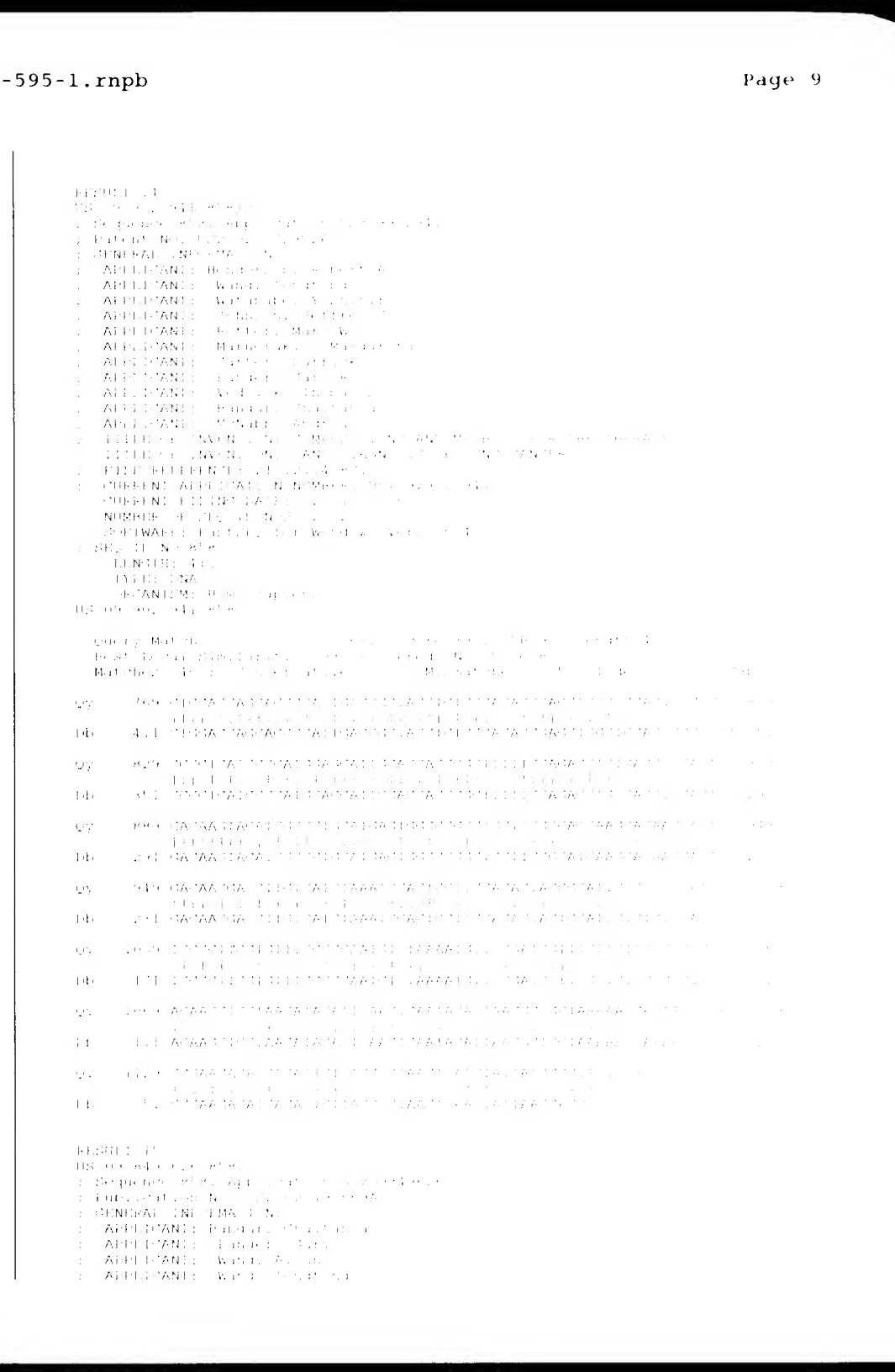

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;  APPLICANT:  Switzer, Anne
;  APPLICANT:  McNeill, Patricia
;  APPLICANT:  Clapper, Jonathan
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C16
;  CURRENT APPLICATION NUMBER:  US/09/340,595
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 1926
;  SOFTWARE: PatentIn for Windows Version 3.0
; SEQ ID NO 858
;    LENGTH: 411
;    TYPE: DNA
;    ORGANISM: Homo sapien
US-09-340-626-858

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Db      411 CTGGACCAGCACCCCATTGACGGGTACCTCTCCCACACCGAGCTGGCTCCACTGCGTGCT 352

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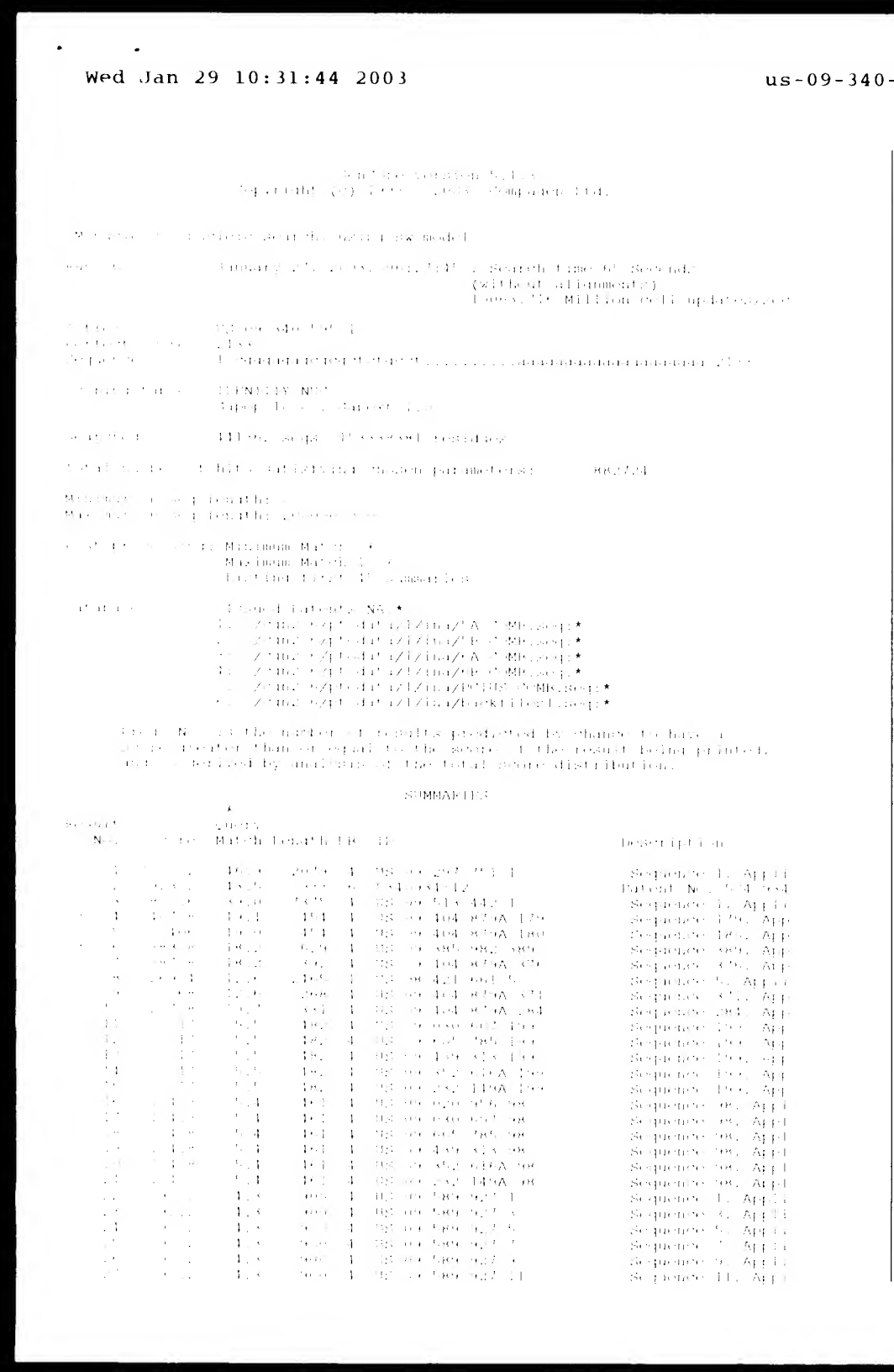

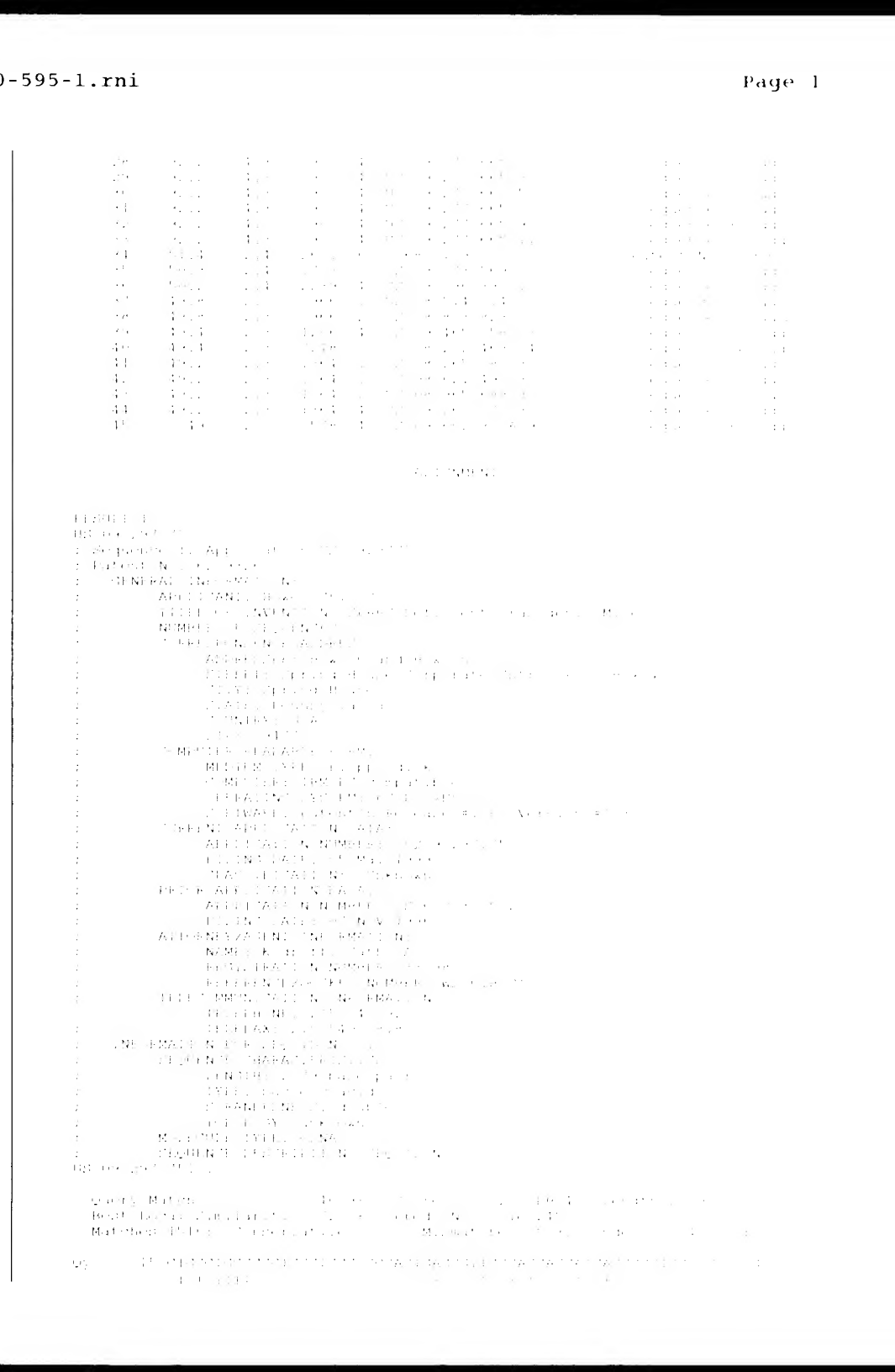

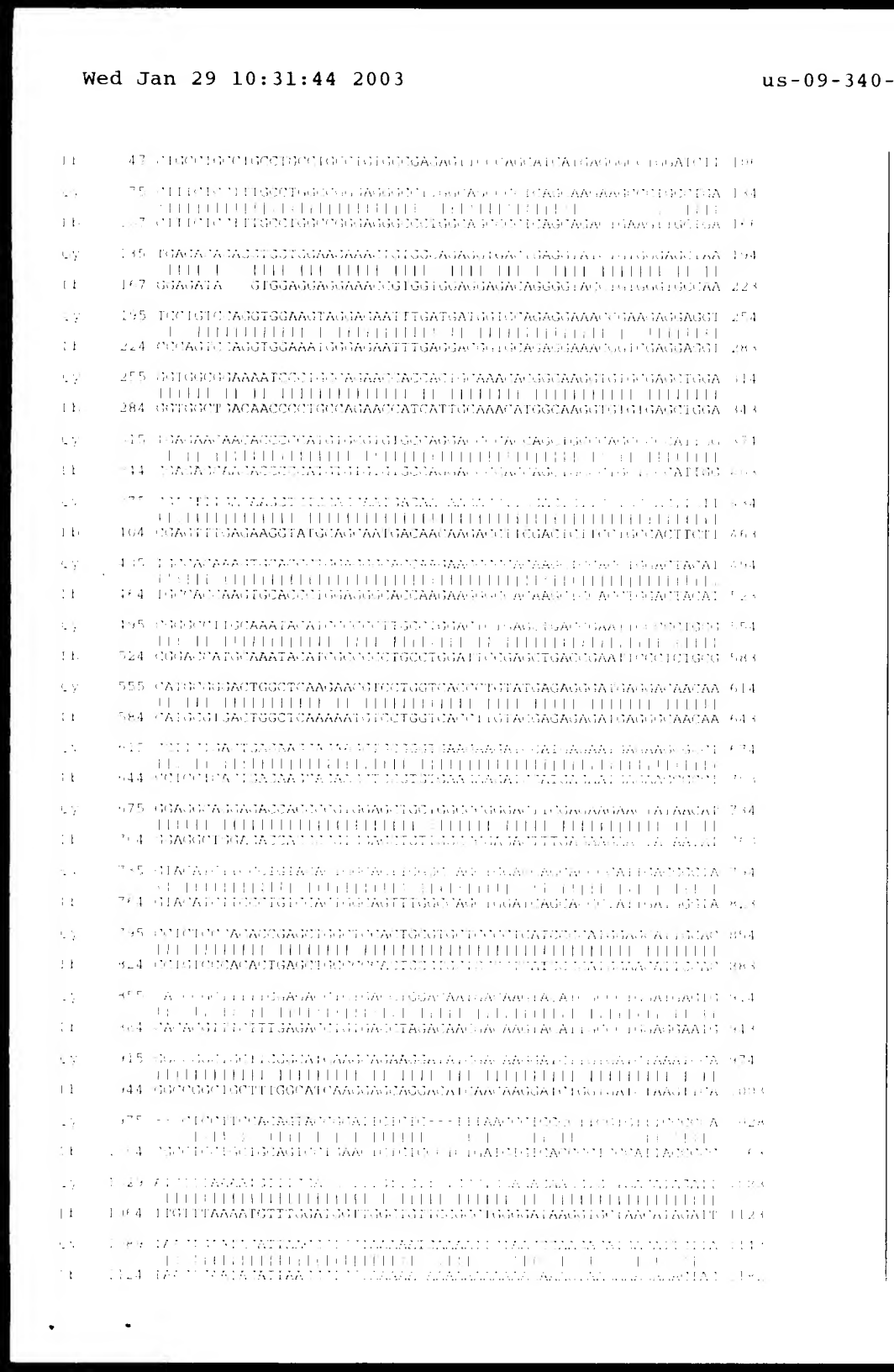

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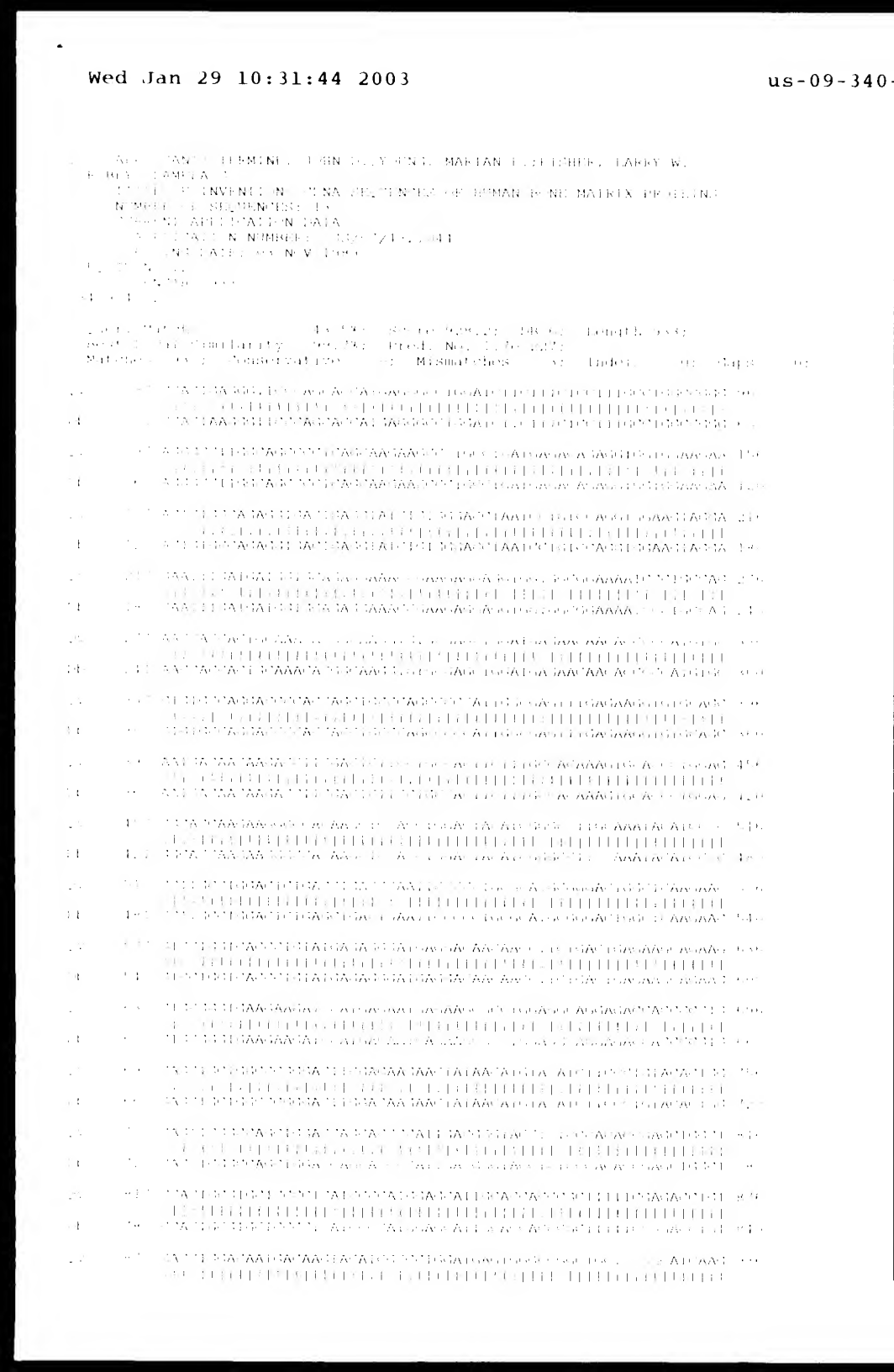
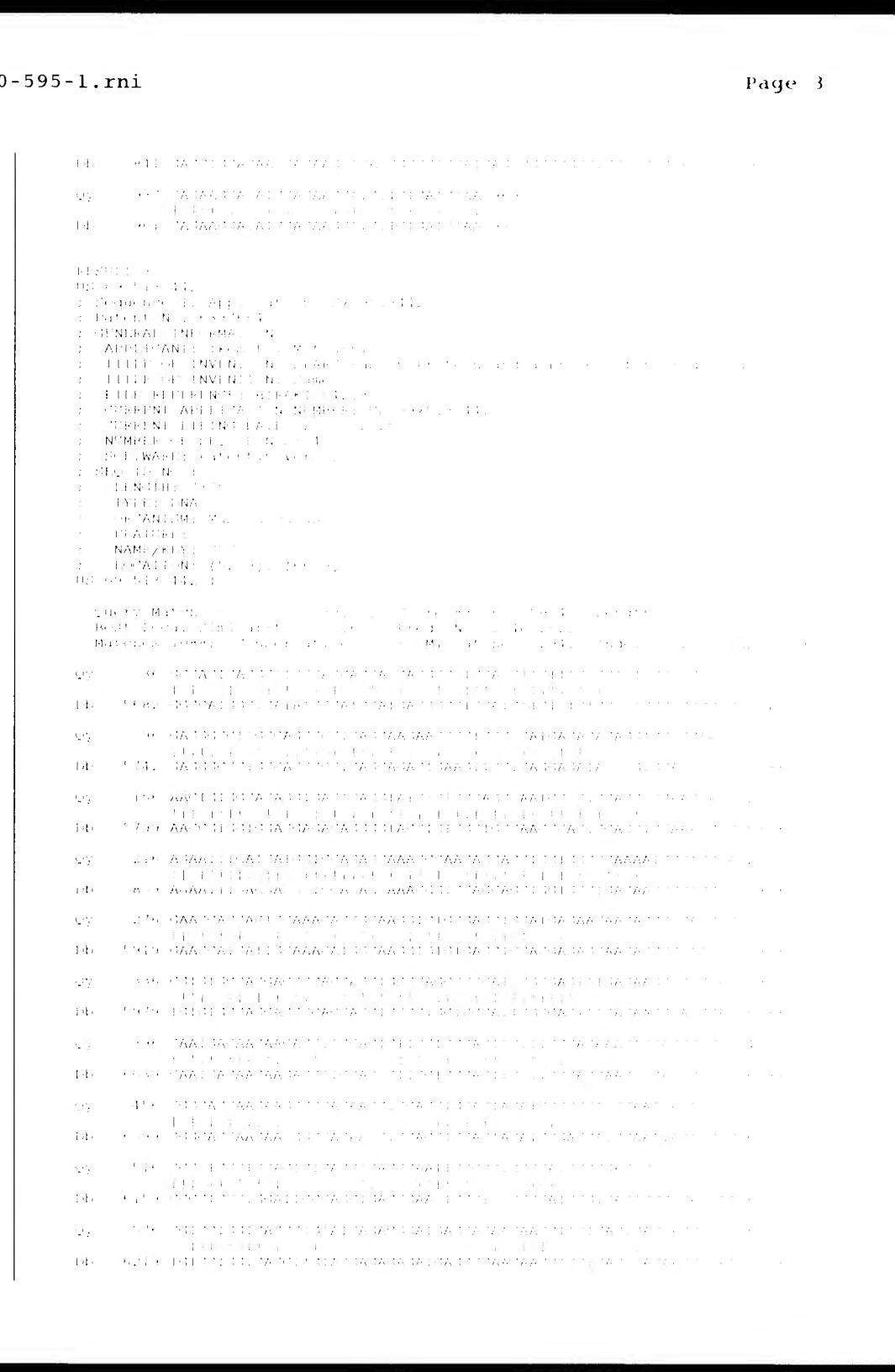
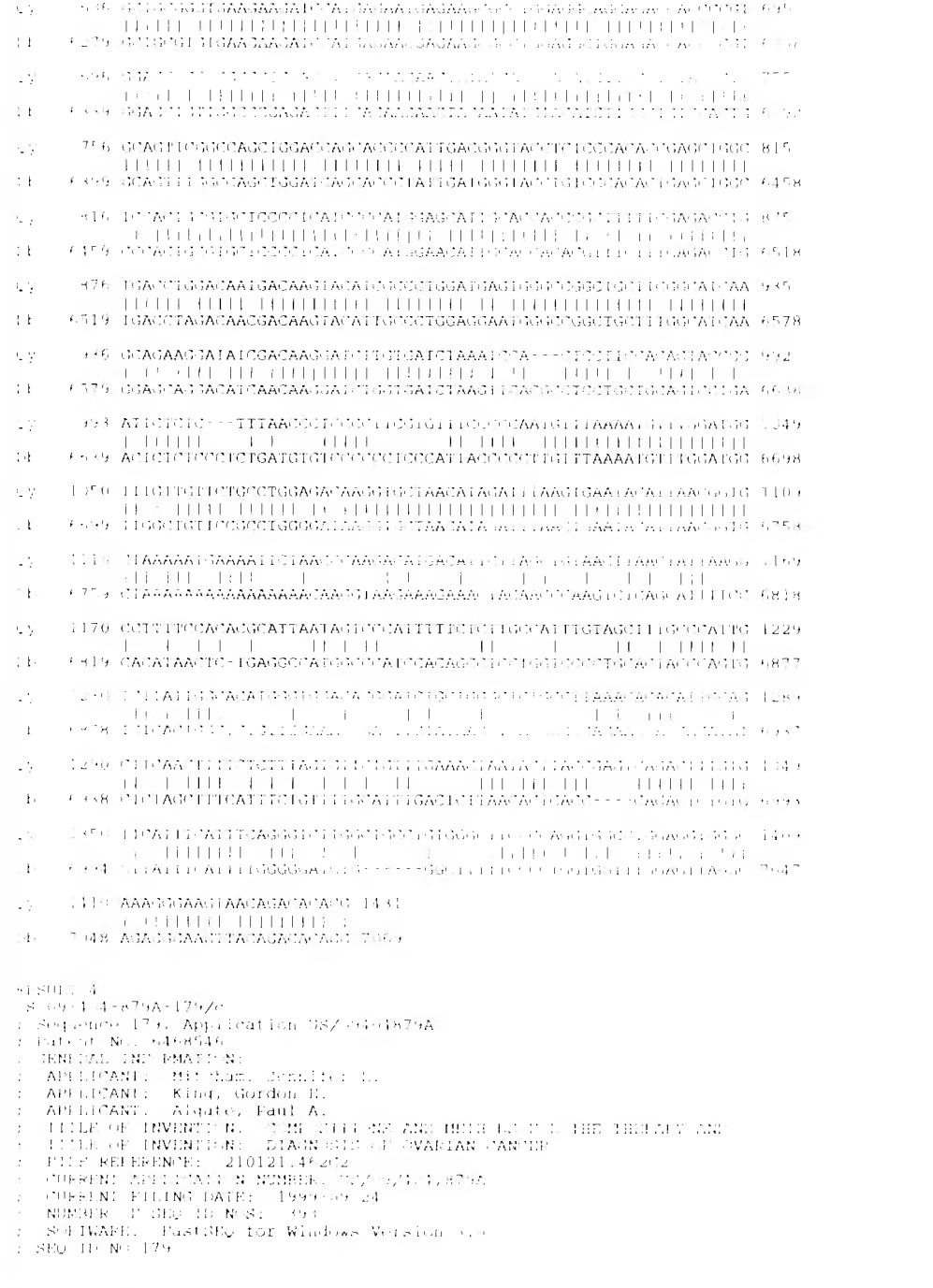
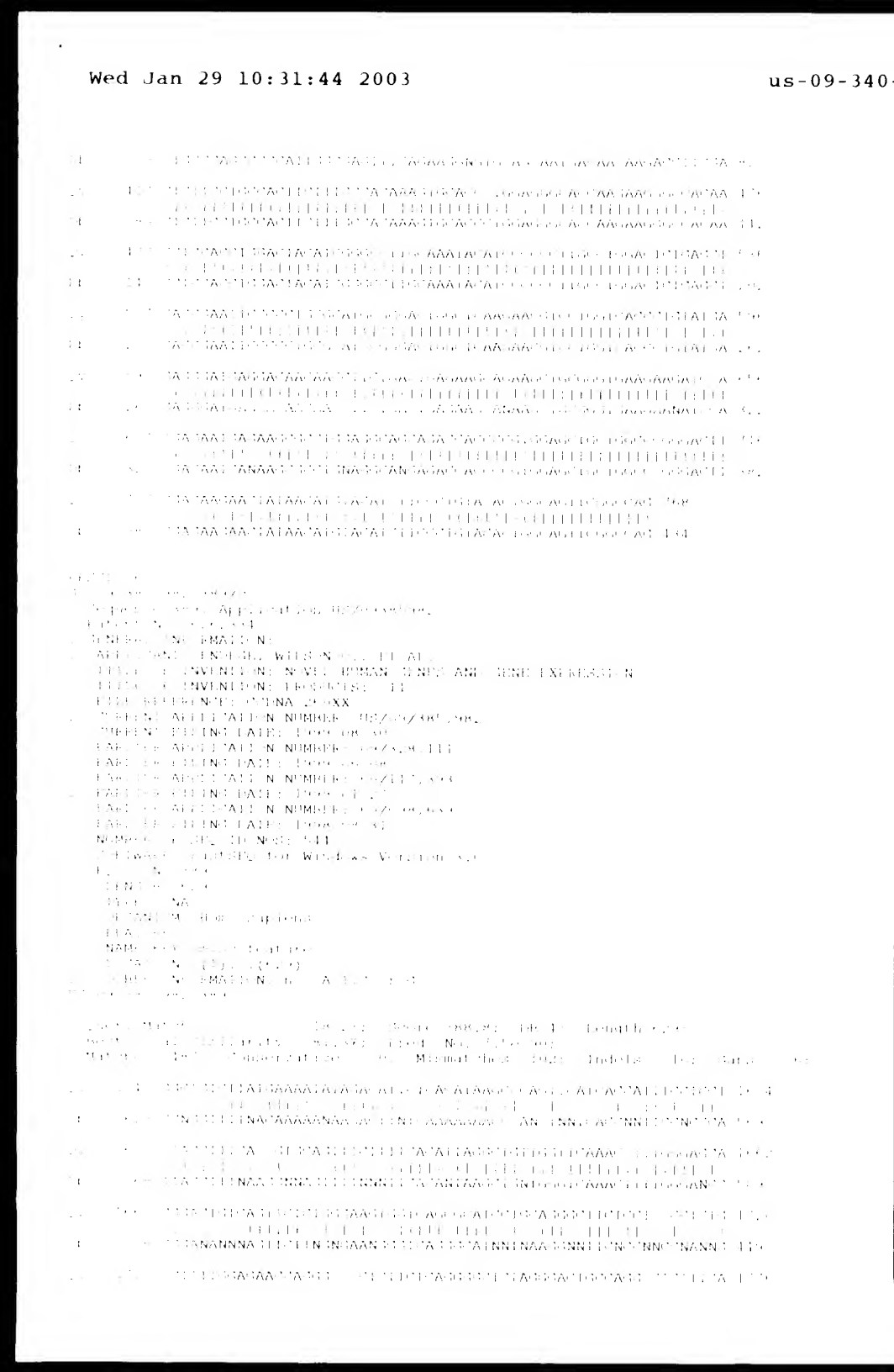
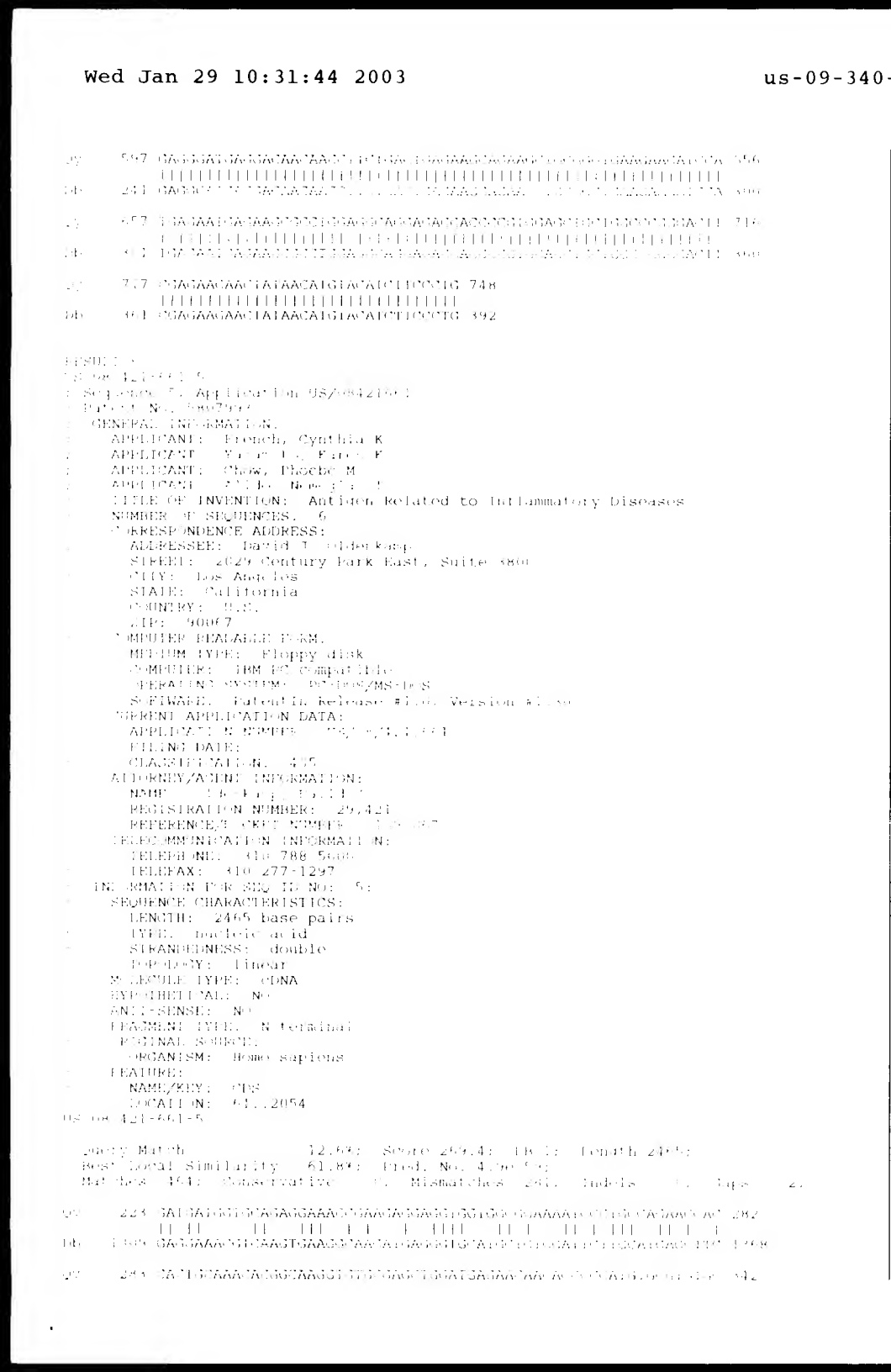
Patent No. 5541311

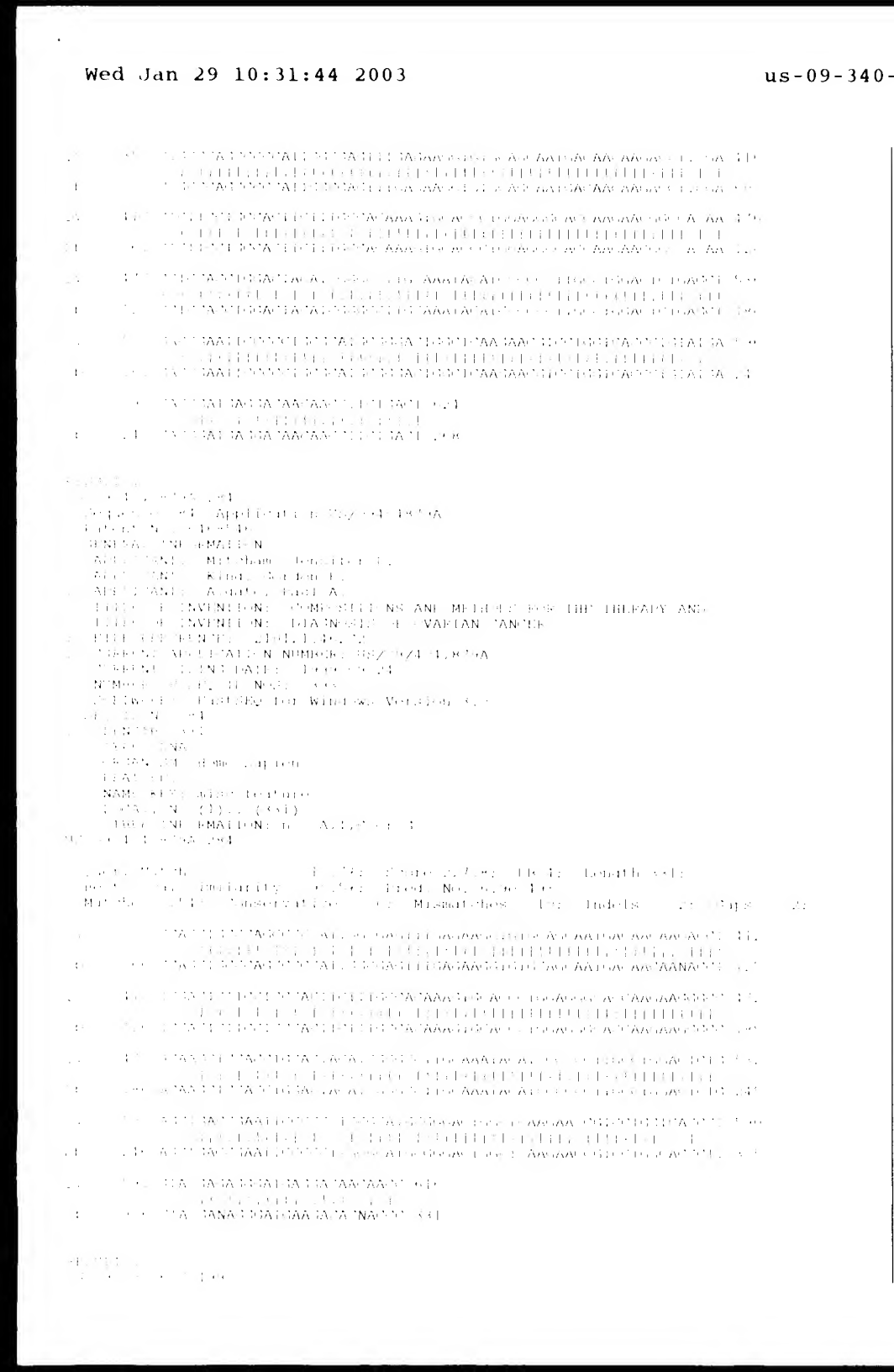












; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Pandit, Gary S.
; APPLICANT: Rotter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Shaikh, Yasir A.W.
; APPLICANT: Hopler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C1C
; CURRENT APPLICATION NUMBER: US/09/005,765
; CURRENT FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 845
; SOFTWARE: PatSEQ for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(482)
; OTHER INFORMATION: n = A,T,C or G
US-09-505-785-199

Query Match 5.5%; Score 117; DB 4; Length 482;
Best Local Similarity 61.5%; Pred. No. 1.7e-29;
Matches 200; Conservative 0; Mismatches 121; Indels 4; Gaps 1;

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Db 87 CTAAATGCAGACTGGAGGGGACCAAAAAGGGGCATCAATCTCAGCTGCATTATTTTGCAG 146

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RESULT 13
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; Sequence 199, Application US/09/149,814
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Pandit, Gary
; APPLICANT: Rotter, Mark
; APPLICANT: Stolk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C2
; CURRENT APPLICATION NUMBER: US/09/149,814
; CURRENT FILING DATE: 1998-09-08
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: PatSEQ for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(482)
; OTHER INFORMATION: n = A,T,C or G
US-09-149-814-199

Query Match 5.5%; Score 117; DB 4; Length 482;
Best Local Similarity 61.5%; Pred. No. 1.7e-29;
Matches 200; Conservative 0; Mismatches 121; Indels 4; Gaps 1;

Qy 389 TTGAGAAGGTGTGCAGCAATGAVCAACAAAJACCTTCGACTCTTCTCTGCCACTTCTTTGCCA 439
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Db 27 TTGATCAAGTTTGTGGCACTGATAATCAAJACCIAIGCIACTIPCTTGPTATCTATTCGCTA 86

Qy 440 CAAAGTGTACCCTGGAJGGCACTAAGAACGGGCAGAAGTTCAVCTGGACTAACTATCAGGG 499
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Db 87 CTAAATGCAGACTGGAGGGGACCAAAAAGGGGCATCAATCTCAGCTGCATTATTTTGCAG 146

Qy 500 CTTGCAAATACATCCCCCCTTGCCTGGACTCTGAGCTGACGGAATTCCCCCTGCGCATGC 559
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Qy 560 GGGAGTGTCTCAAGAACGTCTTGATCAJCCTGTATGAGAGAATGAGTACAAC AAC 615
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Db 207 GAGACTGTCTCAAGAATATCCTGATGCAGCTTTATGAAGCCNATTTGAACACCTGCTT 266

Qy 616 CTTCTGACTCAAAAAAAAAGTTCTTTTCAATAAAATTTAAAAAAAAAAAAAAAAAAA 675
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Db 267 ATTTNAGATGAGAANCAAGAAATAAAATTCNAAAAAATTTAATTTGANAAAAAAGGTTT 326

Qy 676 GAAAAAAAAAAAAAAAAAAAAA 700
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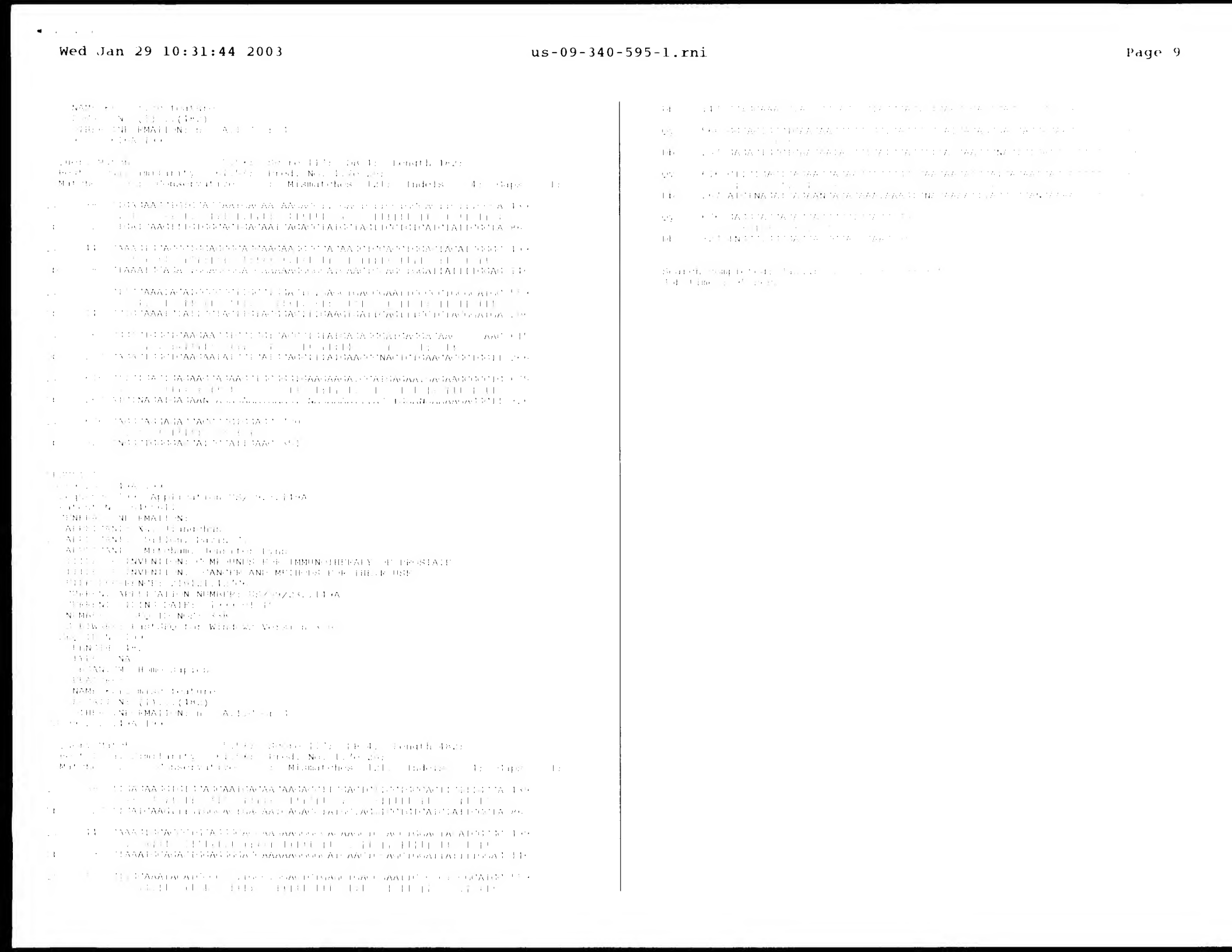
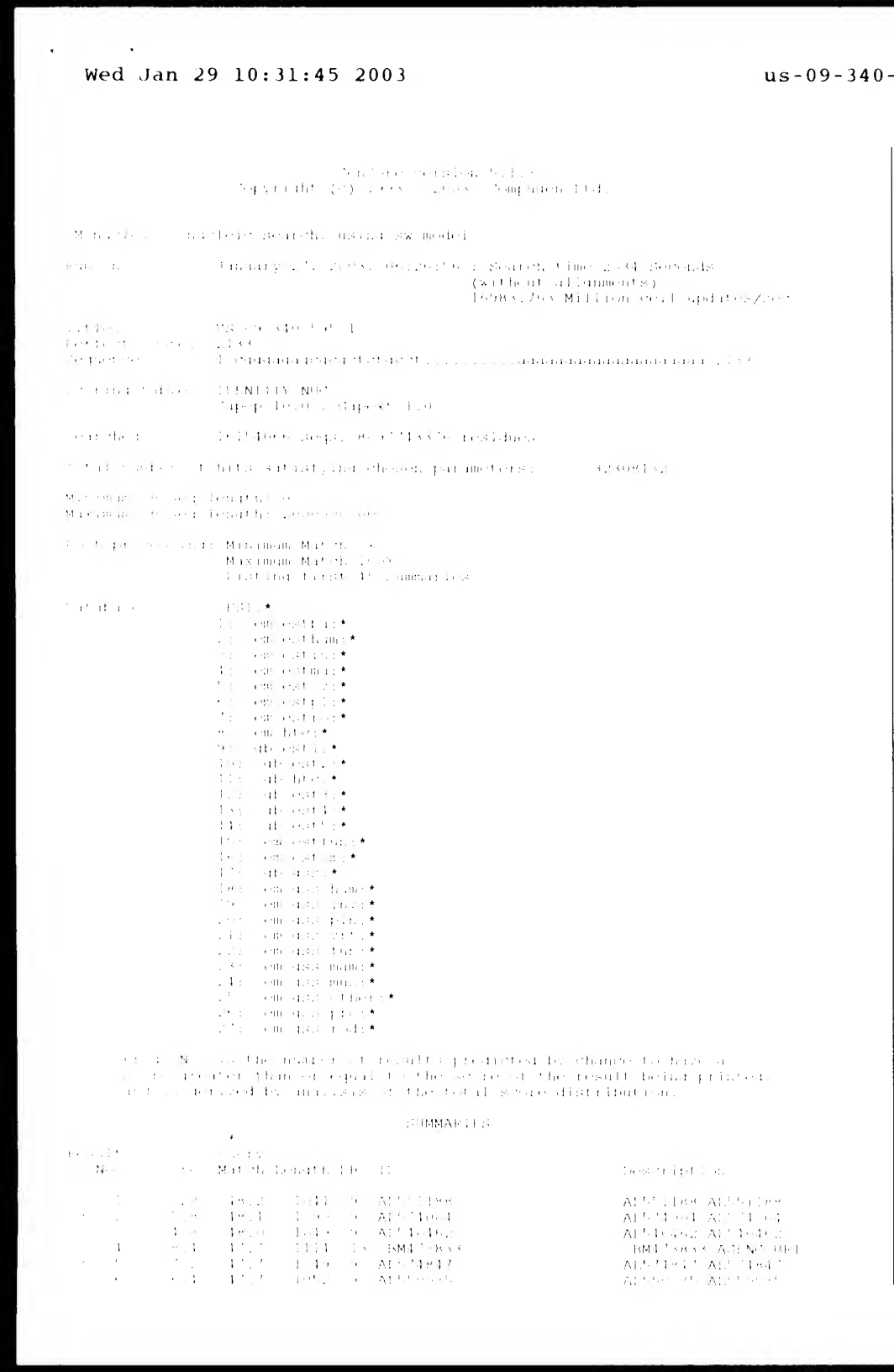
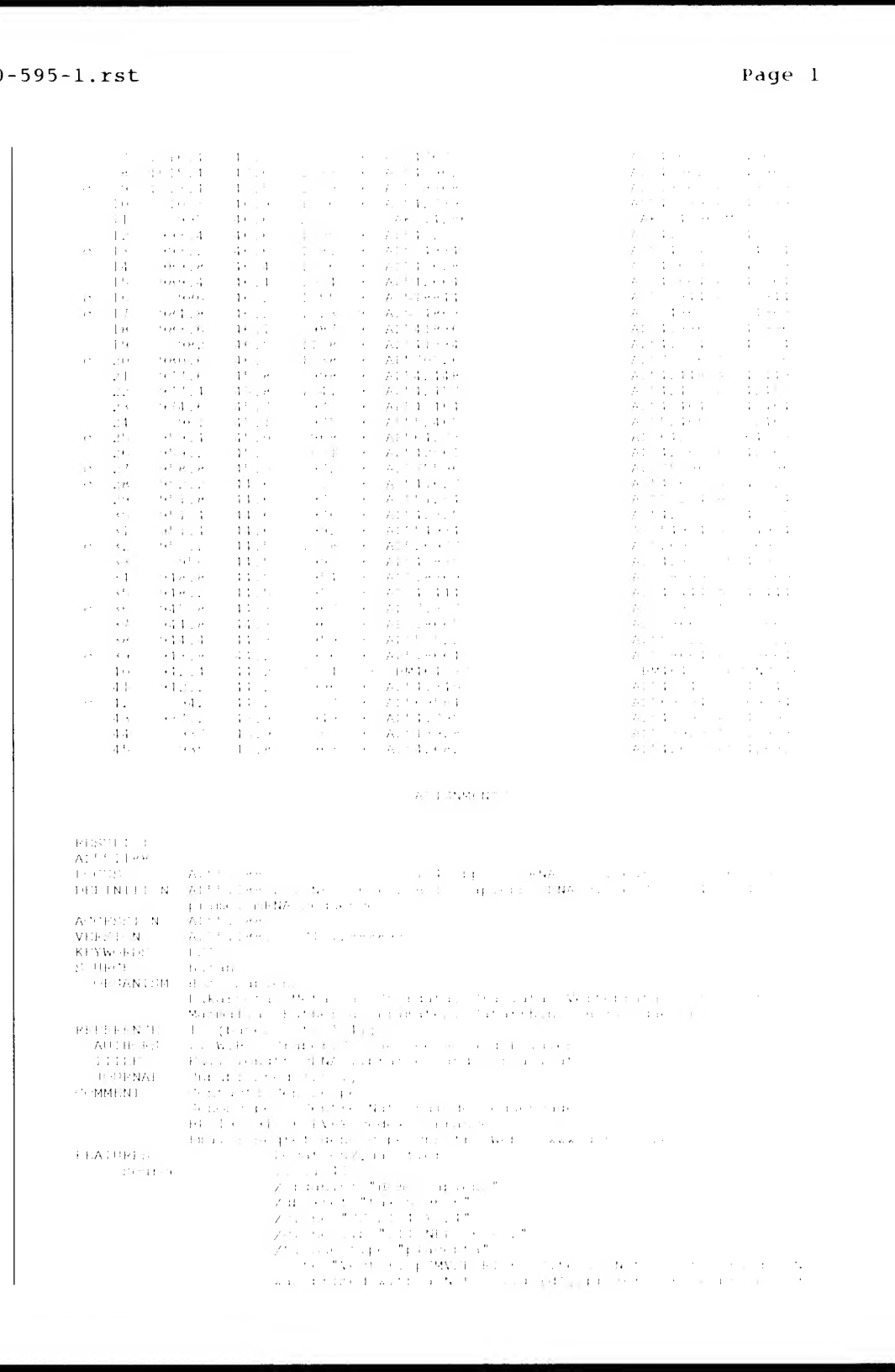
Db 327 TNGGCTGGGGACCATCCCATTGAAC 351

RESULT 14
US-09-352-616A-199
; Sequence 199, Application US/09/352,616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOSITIONS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C3
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: PatSEQ for Windows Version 3.0
; SEQ ID NO 199
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:







enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 240 a 304 c 282 g 214 t 1 others

ORIGIN

Query Match 48.2%; Score 1028; DB 9; Length 1041;
Best Local Similarity 99.8%; Pred. No. 7.7e-157;
Matches 1039; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      18 CCTGCCGCCTGCCTGCCTGCCACTGAGGGTTCCCAGCACCATGAGGGCCTGGATCTTCTT  77
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Db       1 CCTGCCGCCTGCCTGCCTGCCACTGAGGGTT-CCAGCACCATGAGGGCCTGGATCTTCTT  59

Qy      78 TCTCCTTTGCCTGGCCGGGAGGGCCTTGGCAGCCCCTCAGCAAGAAGCCCTGCCTGGATGA 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 TCTCCTTTGCCTGGCCGGGAGGGCCTTGGCAGCCCCTCAGCAAGAAGCCCTGCCTGGATGA 119

Qy     138 GACAGAGGTGGTGGAAGAAACTCTGCCAGAGGTGACTGAGGTATCTCTGTGCGAGCTAATCC 197
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Db     120 GACAGAGGTGGTGGAAGAAACTCTGCCAGAGGTGACTGAGGTATCTCTGTGCGAGCTAATCC 179

Qy     198 TGTCCAGGTGGAAGTAGGAGAATTTGATGATGGTGCAGAGGAAACCGAAGAGGAGGTGGT 257
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Db     180 TGTCCAGGTGGAAGTAGGAGAATTTGATGATGGTGCAGAGGAAACCGAAGAGGAGGTGGT 239

Qy     258 TGCTGAAAATCCCTTCCCAAACTCTACTCTAAAAGAGGAAGATGAAGAGCATCTGGGAGTC 317
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Qy     318 GAAGAACATCCCGCATCTGGTCTCGAGGAGCCTACCAA-GGCAAGCCTGAAGTCGAAGA 376
           ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
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Qy     377 ATTTGAGAAGGTGTTCAAAATAAAGAAGAAAGATTCGAATTTTTGTGAAGTTTTTTGT 436
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Db     360 GTTTGAGAAGGTGTTCAAGAAATAAGAAGAAAGATTCGAATTTTTGTGAAGTTTTTTGT 419

Qy     437 CACAAAGTGCACCCTGGAGGCACCAAGAAGGGCCACAAGCTCCACCTGCACTACATCGG 496
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Db     420 CACAAAGTGCACCCTGGAGGCACCAAGAAGGGCCACAAGCTCCACCTGCACTACATCGG 479

Qy     497 GCCTTGCAAATACATCCGCCCCTTGCCTGGACTCTGAGCTGACCGAATTCCCCCTGGCCAT 556
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Db     480 GCCTTGCAAATACATCCGCCCTTGCCTGGACTCTGAGCTGACCGAATTCCCCCTGGCCAT 539

Qy     557 GGAGGACTGGCTCAAGAACGTCTTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCT 616
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Db     540 GCGGGACTGGCTCAAGAACGTCTTGGTCACCCTGTATGAGAGGGATGAGGACAACAACCT 599

Qy     617 TCTGACTGACAAGCAGAAGCTCGGGGTGAAGAAGATCCATGACAATGATAAGTACAAGCTGA 676
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Db     600 TCTGACTGACAAGCAGAAGCTCGGGGTGAAGAAGATCCATGACAATGATAAGTACAAGCTGA 659

Qy     677 GGCAGGAGACCACCCCGTGGAGCTGCTGGCCCGGGACTTCGATAAGAAGAACTATAACATGTA 736
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Db     660 GGCAGTACAGCAGCCCTGAGTTCCTGTCCCCCGACAGCATCAACAGCAGCTTCAAG 716

Qy     737 CATCTTCCTCTGTACACTGGCAGTTCGGCAGCTGGACGAATTATCTGACTGATGAAGGTAAT 796
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Db     720 CATCTTCCTCTGTACACTGGCAGTTCGGCAGCTGGACGAATTATCTGACTGATGAAGGTAAT 779

Qy     797 CTCCCAGCTCCAGCTCTCTCTATCTCATCTCCTCATCCTCATCTATGATGACTGATGAT 856
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Db     780 CTTCCAGCTCCAGCTCTCTCTATCTCATCTCCTCATCCTCATCTATGATGACTGATGAT 839

Qy     857 GGGCTTTTTCGACAGCTCTCTGTATGTATGAGCTTCTCTTTGTTCTTTTTTTTTTTTTT 916
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Db     840 GGGCTTTTTCGACAGCTCTCTGTATGTATGAGCTTCTCTTTGTTCTTTTTTTTTTTTTT 899
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RESULT 2
AL574004/c
LOCUS AL574004 1690 bp mRNA linear rod 07-JUN-2001
DEFINITION AL574004.1 IMAGE:4111_NF1000_F12 Homo sapiens cDNA clone IMAGE:4111_NF1000_F12 5', mRNA sequence.
ACCESSION AL574004
VERSION AL574004.1 GI:13124703
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1690)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4111-NF1000-21"
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Size separated cDNA enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 441 a 238 c 244 g 266 t 1 others
ORIGIN

Query Match 48.1%; Score 1025.8; DB 9; Length 1690;
Best Local Similarity 98.6%; Pred. No. 8.2e-157;
Matches 1054; Conservative 2; Mismatches 9; Indels 4; Gaps 2;

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Qy     978 CTCCAGCTCTCTCTATCTCATCTCCTCATCCTCATCTATGATGACTGATGATGGGCTTT 1037
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Db    1471 CTCCAGCTCTCTCTATCTCATCTCCTCATCCTCATCTATGATGACTGATGATGGGCTTT 1530

Qy    1038 TTCGACAGCTCTCTGTATGTATGAGCTTCTCTTTGTTCTTTTTTTTTTTTTT 1090
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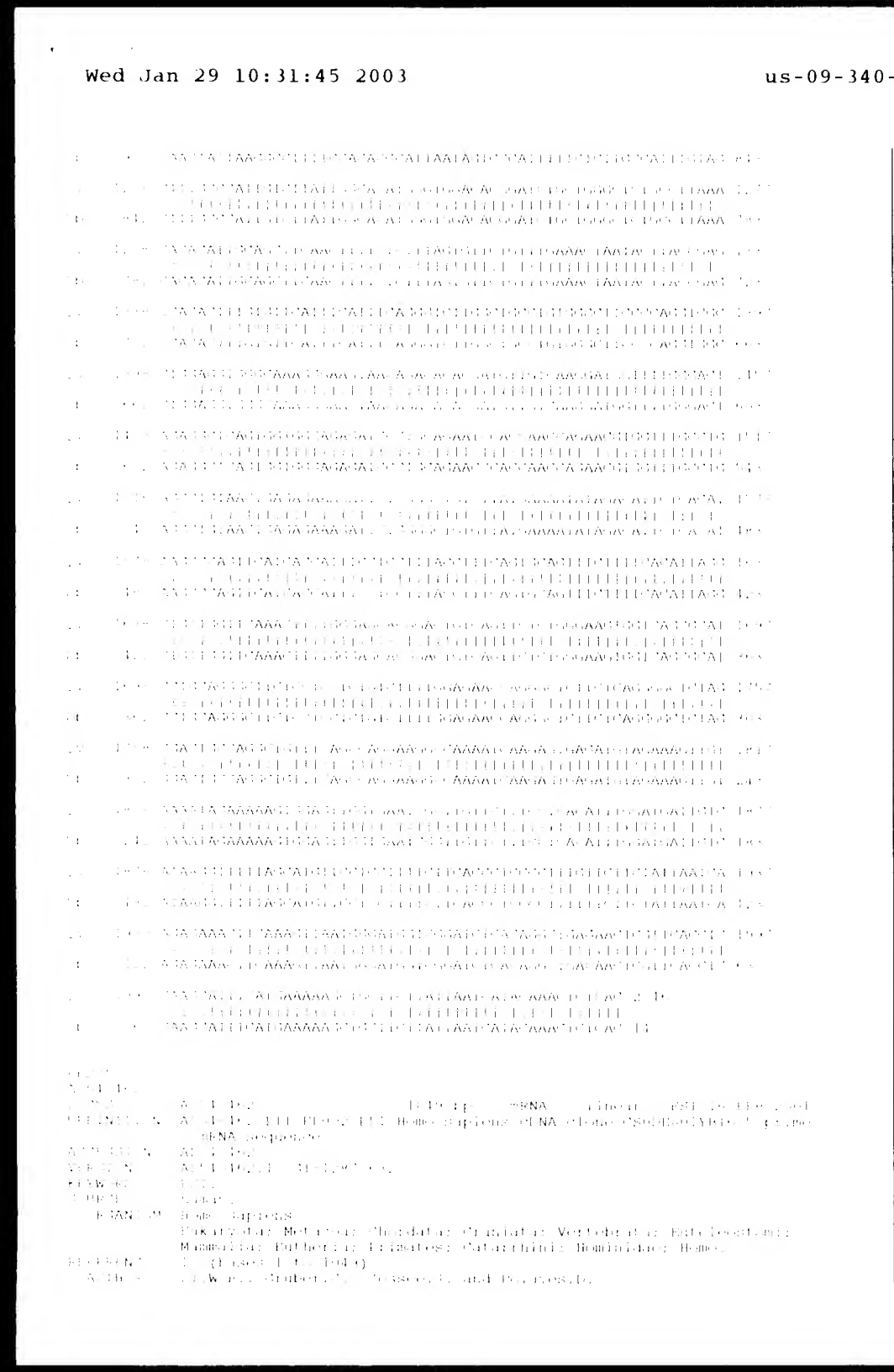

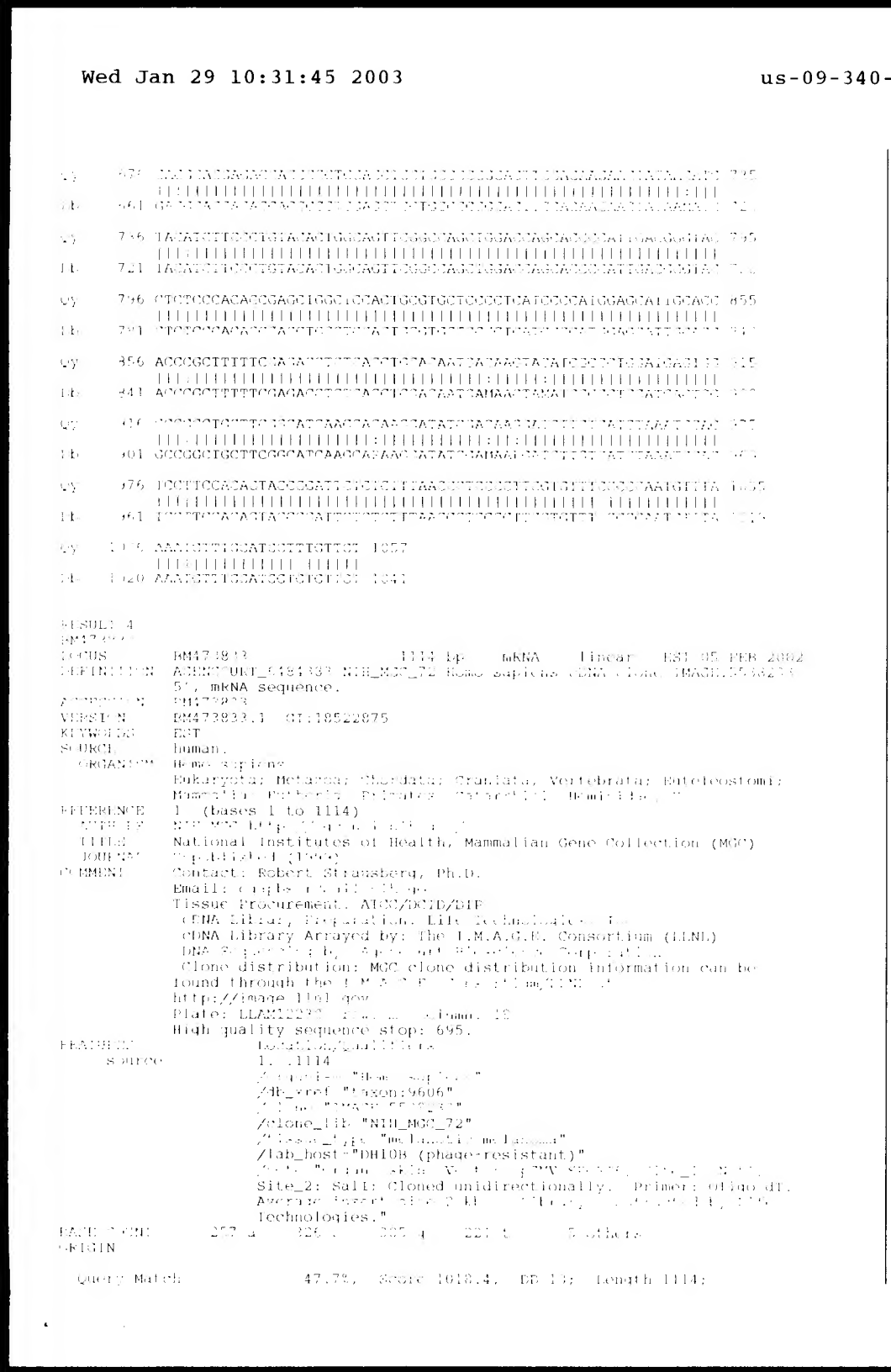

RESULT 4
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LOCUS BM473833 1114 bp mRNA linear EST 05-FEB-2002
DEFINITION AI302700.xb1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2552254
5', mRNA sequence.
ACCESSION BM473833
VERSION BM473833.1 GI:18522875
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
REFERENCE 1 (bases 1 to 1114)
AUTHORS [illegible]
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DIP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: [illegible]
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL clone
http://image.llnl.gov
Plate: LLAM12238 Row: [illegible] Column: 12
High quality sequence stop: 695.
FEATURES Location/Qualifiers
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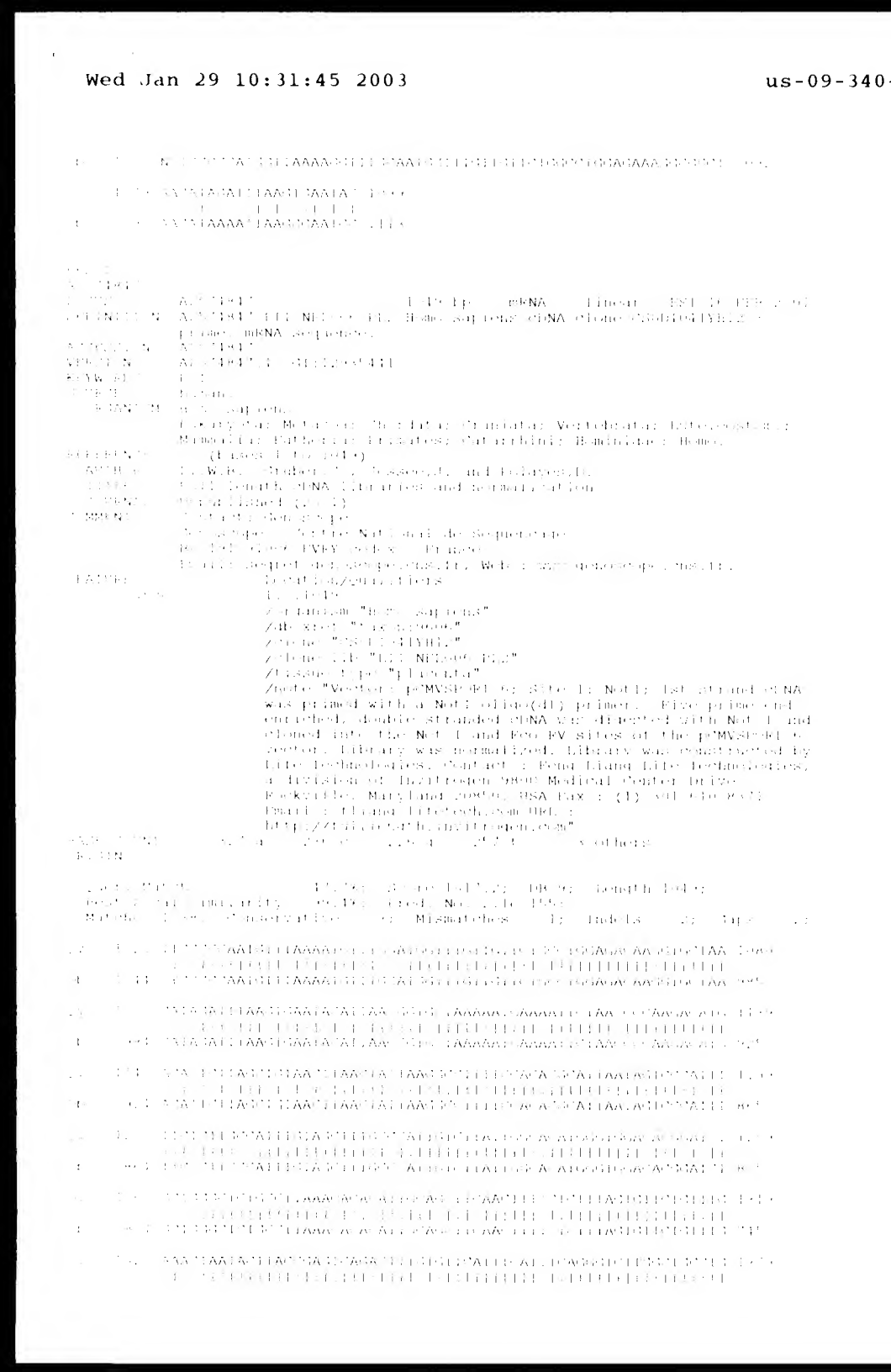
/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="male"
/clone_lib="NIH_MGC_72"
/clone="IMAGE:2552254"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pCMV-SPORT6; CloneID: 2552254;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size: 2 kb; Single pass sequenced; 5'
Technologies."
BASE COUNT 257 a 326 c 335 g 221 t 5 others
ORIGIN

Query Match 47.7%, Score 1018.4, DB 13; Length 1114;
Best Local Similarity 96.9%; Pred. No. 1.6e-159;
Matches 1097; Conservative 0; Mismatches 31; Indels 4; Gaps 1;



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/db_xref="taxon:9606"
/clone="CS0DI053YO21"
/clone_lib "LLL_NF5606_HL2"
/tissue_type "placenta"
/note "Vector: pCMVSPORT 6; Site 1: Not I; Site 2: cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 241 a 309 c 289 g 213 t 1 n
ORIGIN

Query Match 47.7%; Score 1016.4; DB 9; Length 1052;
Best Local Similarity 98.5%; Pred. No. 2.8e-155;
Matches 1036; Conservative 1; Mismatches 12; Indels 3; Gaps 1;

Qy 1 CGGGAGAGCGCGCTCTGCCTGCCGCCTGCCTGCCTGCCACTGAGGCTTCCCAGCACCATG 60
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Db 4 CGGGAGAGCGCGCTCTGCCTGCCGCCTGCCTGCCTGCCACTGAGGCTTCCCAGCACCATG 63

Qy 61 AGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGCAGGGCCTTGGCAGCCGCTCAGCAA 120
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Db 64 AGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGCAGGGCCTTGGCAGCCGCTCAGCAA 123

Qy 121 GAAGCCCTGCCTGATGAGACAGAGGTGGTGGAAGAAACTGTGGCAGACGTGACTGAGGTA 180
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Db 124 GAAGCCCTGCCTGATGAGACAGAGGTGGTGGAAGAAACTGTGGCAGACGTGACTGAGGTA 183

Qy 181 CCTCTTTCAAGTTAATCCTGTCTCAGCTCGAAGTAGCAGAATTTGAGATGATGGTGCAGAGGAA 240
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Db 244 ATTGAAATAGAGTGTGTTTCTTGAAATCCTTGCTAAATCTCATAGTGGAGTGATTTTTGTAA 303

Qy 301 CCAGCCCCGATTGGCGAGTTTGAGAAGCTGTGCATAATACAATAGAAGCTCAGATTT 420
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Db 304 CCAGCCCCGATTGGCGAGTTTGAGAAGCTGTGCATAATACAATAGAAGCTCAGATTT 423

Qy 421 TCCTGCCTCTCTTTCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 480
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Db 424 TCCTGCCTCTCTTTCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 483

Qy 481 CAGCTGGACTACATCGGGCCTGTGAAAATAGATCCCCCTTGCCTGGACTCTGAGCTGAGC 540
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Db 484 CAGCTGGACTACATCGGGCCTGTGAAAATAGATCCCCCTTGCCTGGACTCTGAGCTGAGC 543

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Qy 601 GAGAGTAAAAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 660
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Qy 661 AAAAAAAAGCCCCTGGAAGTGAGAGAGAGTTTTTTGGAATTTTTGGGTTTTTAAAGTTTTT 720
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Db 664 AATTAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 723

Qy 721 AAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 780
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Qy 781 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 840
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Qy 841 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 900
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Qy 901 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 960
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Qy 961 GTGATTTAAAATTTACTCTTTCTATGTATGTTTGATTTTTAATTTTTTTTTTTTTTTTTT 1020
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Db 964 GTGATTTAAAATTTACTCTTTCTATGTATGTTTGATTTTTAATTTTTTTTTTTTTTTTTT 1023

Qy 1021 TTTTTTTTAAATTTTAAAATTTTTTGTATGTTTT 1052
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Db 1024 TTTTTTTTAAATTTTAAAATTTTTTGTATGTTTT 1055

RESULT 7
AL547671
LOCUS AL547671 1057 bp mRNA linear EST. 3-JUN-2
DEFINITION AL547671 LLL_NF5606_HL2 Homo sapiens cDNA clone CS0DI053YO21 5-prime, mRNA sequence.
ACCESSION AL547671
VERSION AL547671.1 GI:12881950
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE 1 (bases 1 to 1057)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 cedex - France
Email: segret@genoscope.cns.fr, WWW : www.genoscope.cns.fr.
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/tissue_type "placenta"
/note "Vector: pCMVSPORT 6; Site 1: Not I; Site 2: cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 287 a 228 c 229 g 312 t 1 others
ORIGIN

Query Match 47.7%; Score 1016.4; DB 9; Length 1057;
Best Local Similarity 98.5%; Pred. No. 2.8e-155;
Matches 1036; Conservative 1; Mismatches 12; Indels 3; Gaps 1;

Qy 1 CGGGAGAGCGCGCTCTGCCTGCCGCCTGCCTGCCTGCCACTGAGGCTTCCCAGCACCATG 60
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Db 4 CGGGAGAGCGCGCTCTGCCTGCCGCCTGCCTGCCTGCCACTGAGGCTTCCCAGCACCATG 63

Qy 61 AGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGCAGGGCCTTGGCAGCCGCTCAGCAA 120
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Db 64 AGGGCCTGGATCTTCTTTCTCCTTTGCCTGGCCGGCAGGGCCTTGGCAGCCGCTCAGCAA 123

Qy 121 GAAGCCCTGCCTGATGAGACAGAGGTGGTGGAAGAAACTGTGGCAGACGTGACTGAGGTA 180
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Db 124 GAAGCCCTGCCTGATGAGACAGAGGTGGTGGAAGAAACTGTGGCAGACGTGACTGAGGTA 183

Qy 181 CCTCTTTCAAGTTAATCCTGTCTCAGCTCGAAGTAGCAGAATTTGAGATGATGGTGCAGAGGAA 240
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Db 184 TCTGTGGGAGCTAATCCTGTCCAGGTGGAAGTAGCAGAATTTGAGATGATGGTGCAGAGGAA 243

Qy 241 ATTAACAGAGAGTGTGTTTCTTGAAATCCTTGCTAAATCTCATAGTGGAGTGATTTTTGTAA 300
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Qy 301 CCAGCCCCGATTGGCGAGTTTGAGAAGCTGTGCATAATACAATAGAAGCTCAGATTT 420
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Db 304 CCAGCCCCGATTGGCGAGTTTGAGAAGCTGTGCATAATACAATAGAAGCTCAGATTT 423

Qy 421 TCCTGCCTCTCTTTCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 480
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Db 424 TCCTGCCTCTCTTTCTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 483

Qy 481 CAGCTGGACTACATCGGGCCTGTGAAAATAGATCCCCCTTGCCTGGACTCTGAGCTGAGC 540
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Qy 541 GAACTCCTCCTGTGCATCCTGACTGGTGAAGAACTCTGTGCTGCCAGTTCTATCAGAGAA 600
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Db 544 GAACTCCTCCTGTGCATCCTGACTGGTGAAGAACTCTGTGCTGCCAGTTCTATCAGAGAA 603

Qy 601 GAGAGTAAAAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 660
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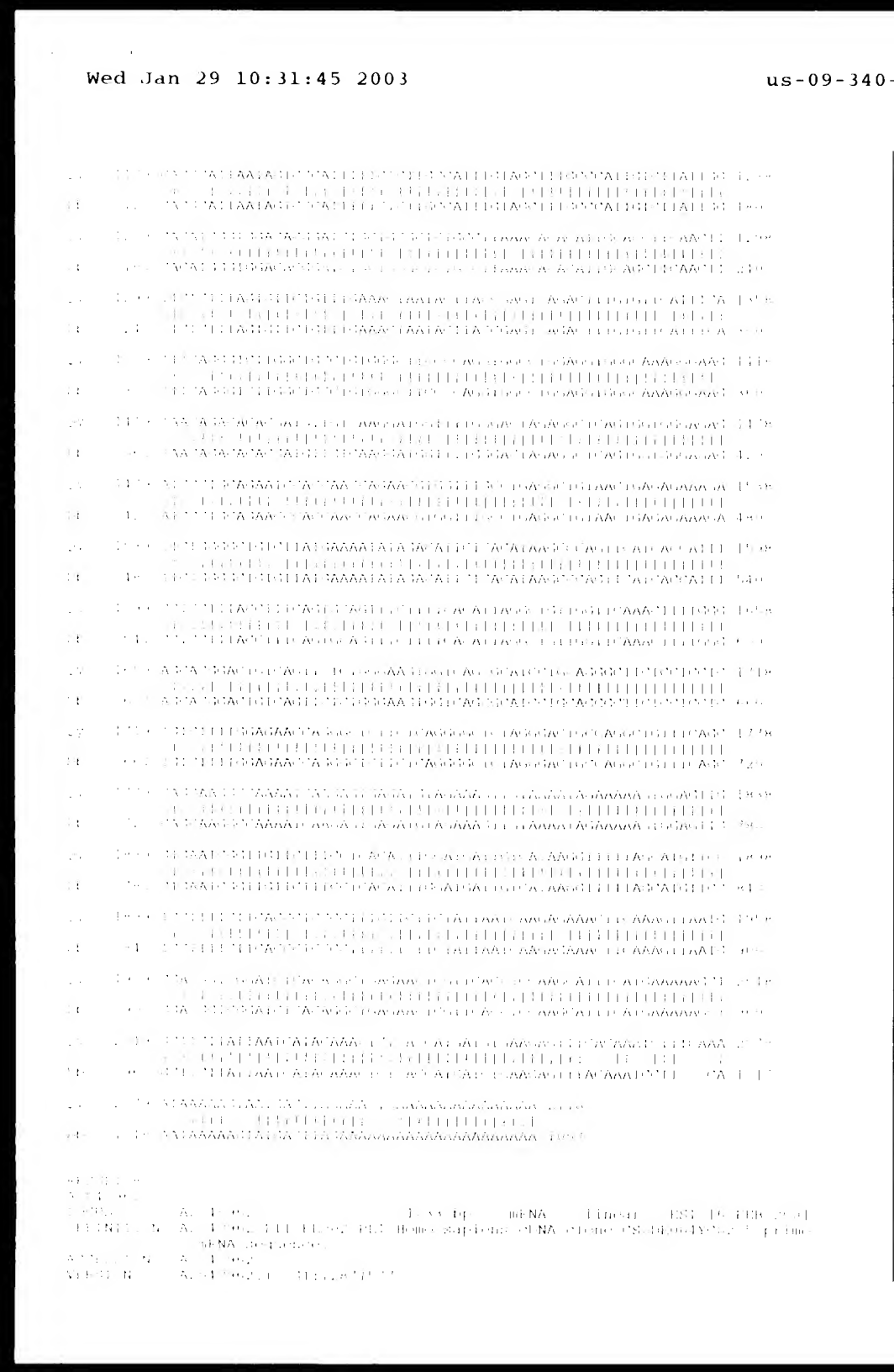

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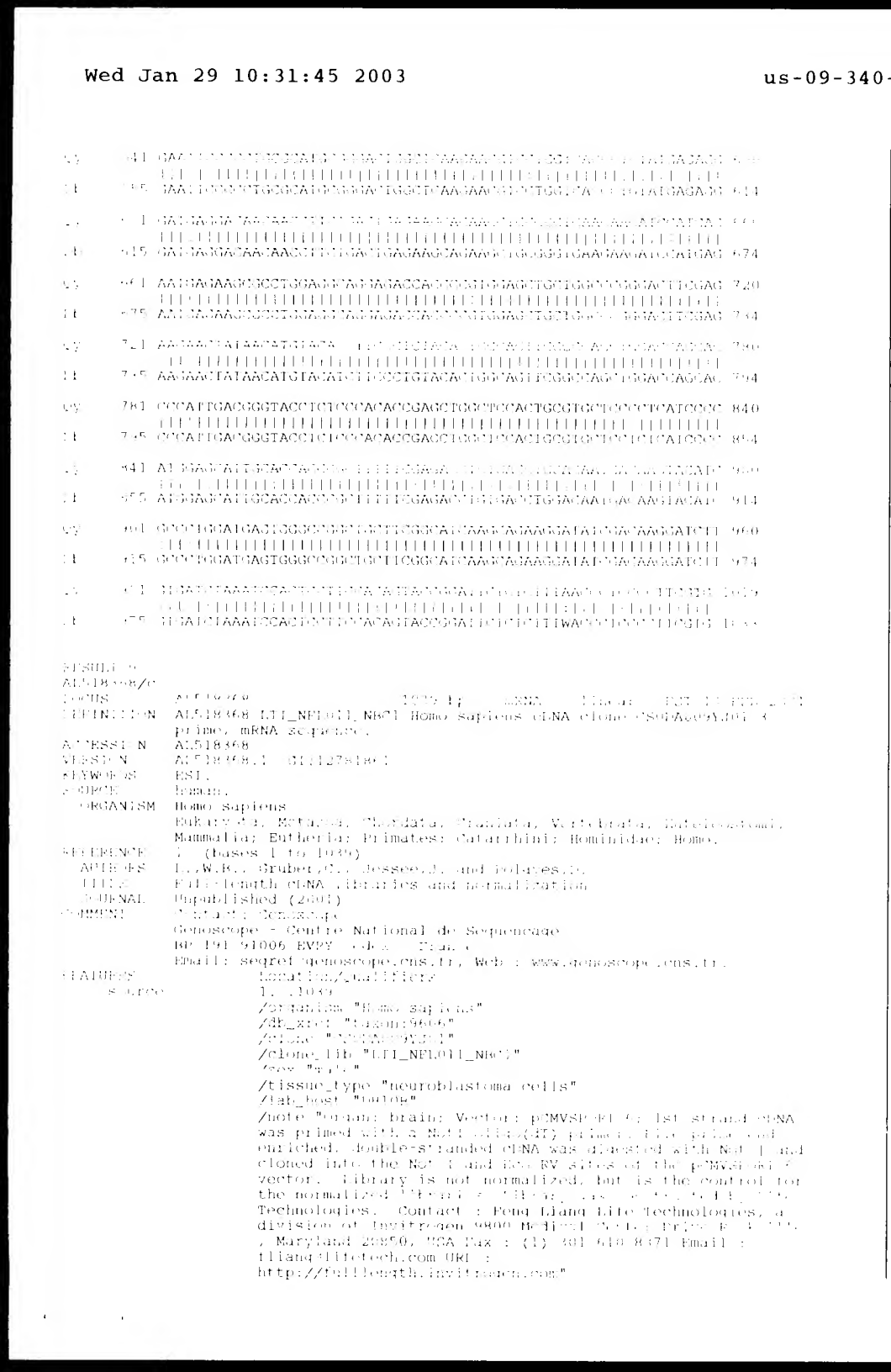

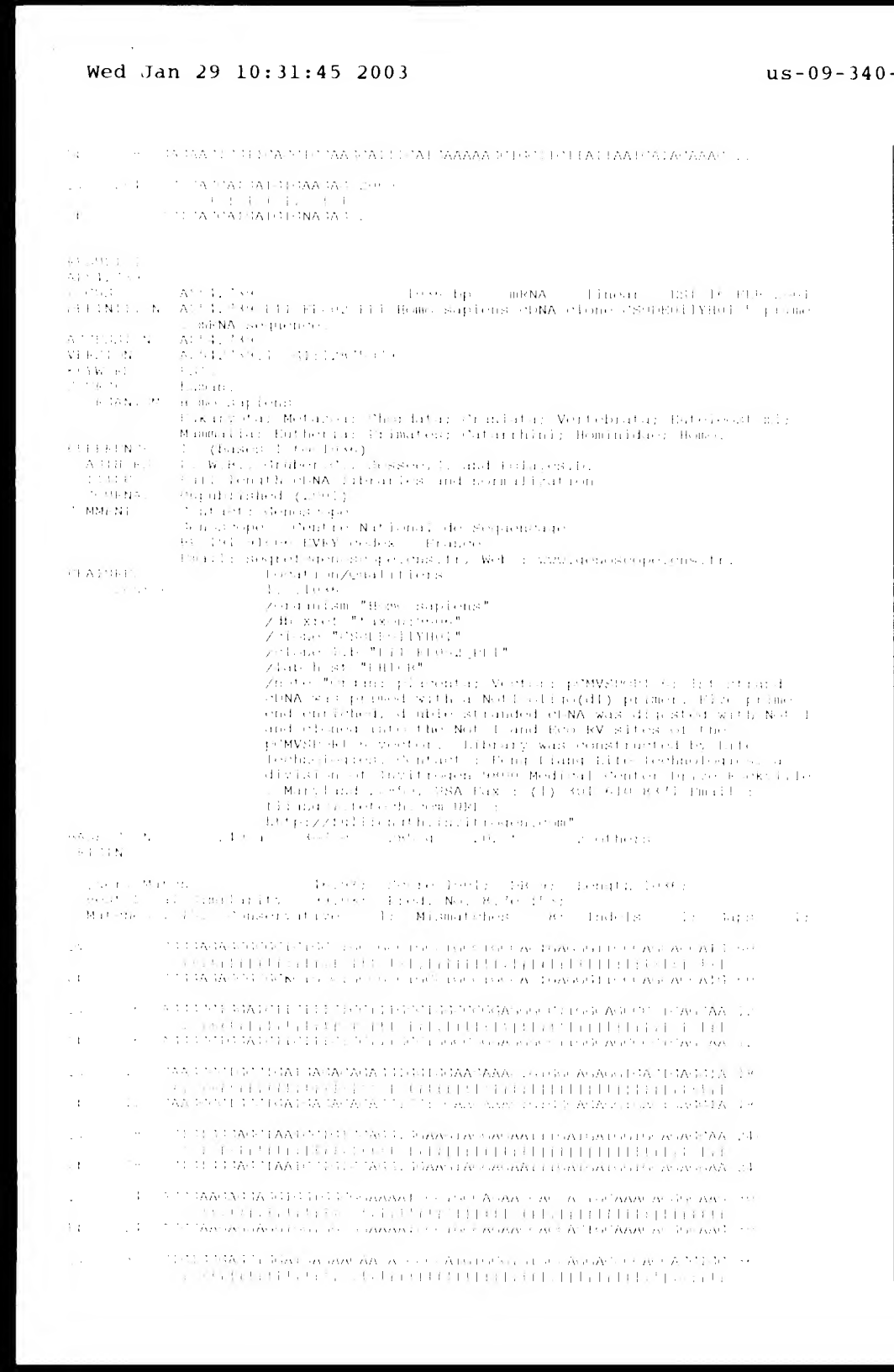

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  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
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REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Hara,A.,
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            Yoneda,Y., Ishikawa,I., Kuroda,K., Tanaka,T., Matsuura,S., Kitajima,S.,
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  TITLE     RIKEN integrated sequence anal,sis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20540013
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REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
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            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
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REFERENCE   5  (bases 1 to 2101)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akiyama,J., Amid,A., Andrade,A.,
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            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-NOV-2001) Y. Hayashizaki, Physical and Chemical
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Yokohama Institute, Genome Science
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:yosi@gsc.riken.go.jp, URL:http://
            URL:http://, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
  COMMENT   Please visit our web site (http://...) for
            further details.
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            Division of Experimental Animal System in RIKEN ...
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            and subsequently captured by cap trapper. Both ...
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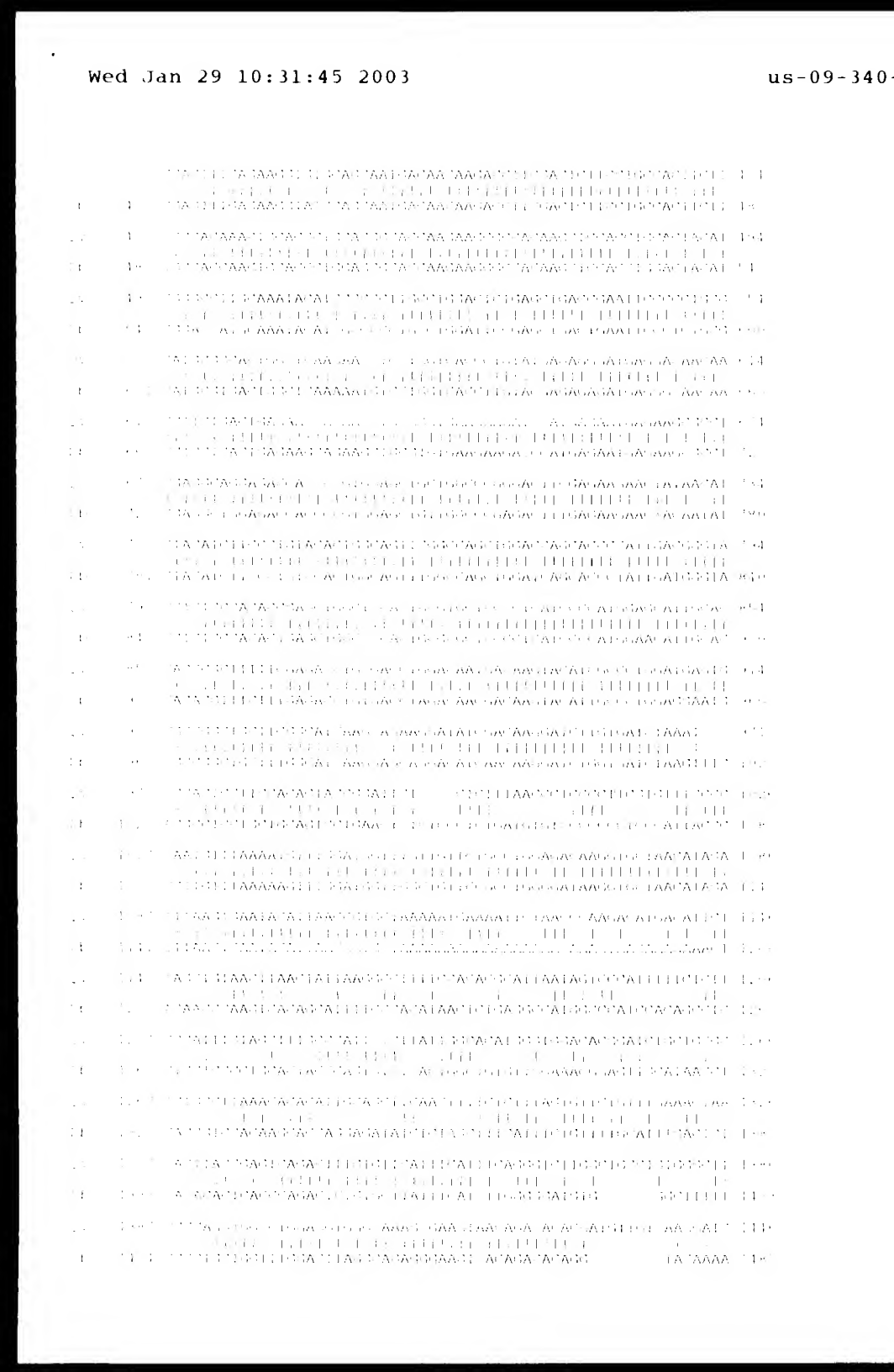

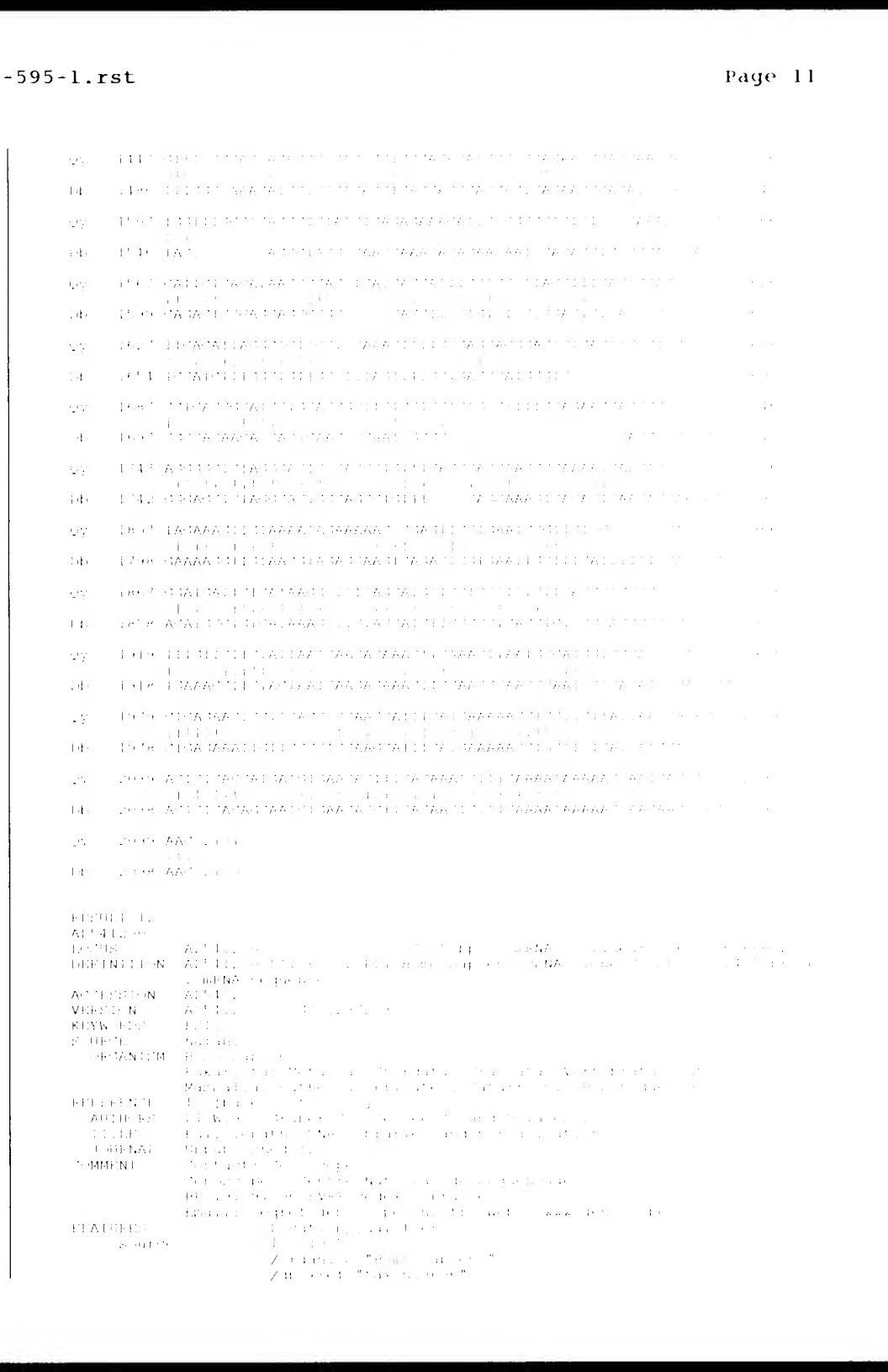

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BASE COUNT 232 a 297 c 227 g 197 t 2 others
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Query Match 46.6%; Score 993.4; DB 9; Length 1805;
Best Local Similarity 99.5%; Pred. No. 1.5e-151;
Matches 694; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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BASE COUNT 232 a 297 c 227 g 197 t 2 others
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Query Match 46.6%; Score 993.4; DB 9; Length 1805;
Best Local Similarity 99.5%; Pred. No. 1.5e-151;
Matches 694; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 1061)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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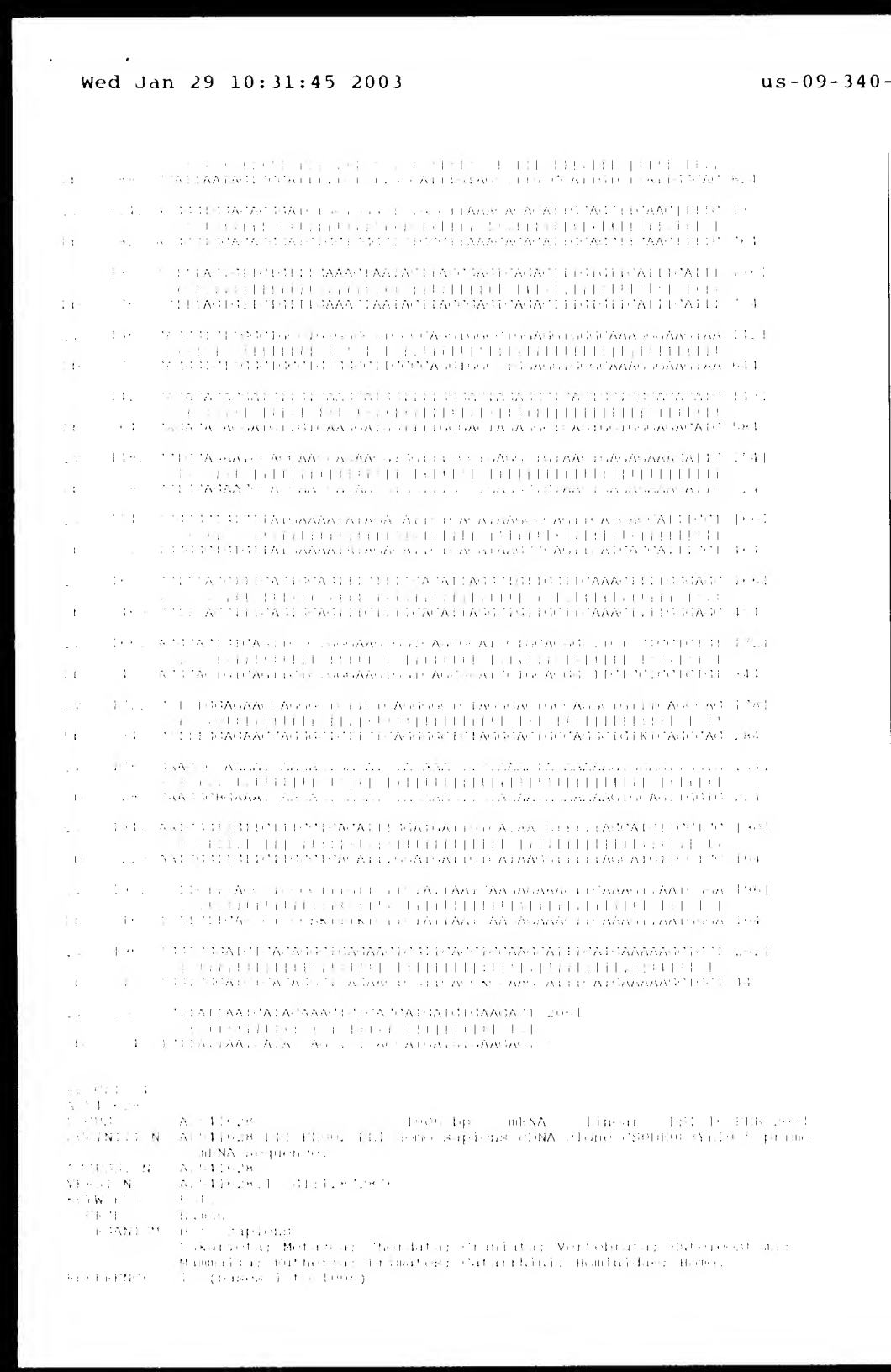

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DEFINITION AI542664 EST_FL002_H11 Homo sapiens cDNA clone 2S00E014Y02 5' prime, mRNA sequence.
ACCESSION AI542664
VERSION AI542664.1 GI:12871942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1034)
AUTHORS [illegible]
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secret@genoscope.cns.fr, Web : [illegible]
FEATURES Location/Qualifiers
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/clone="2S00E014Y02"
/clone_lib="fli_fl002_H11"
/lab_host="DH10B"
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BASE COUNT 236 a 319 c 283 g 206 t 190 others
ORIGIN

Query: Match 46.4%; Score 289.4; DB 9; Length 1034;
Best Local Similarity 99.2%; Prob. No. 6.6e-151;
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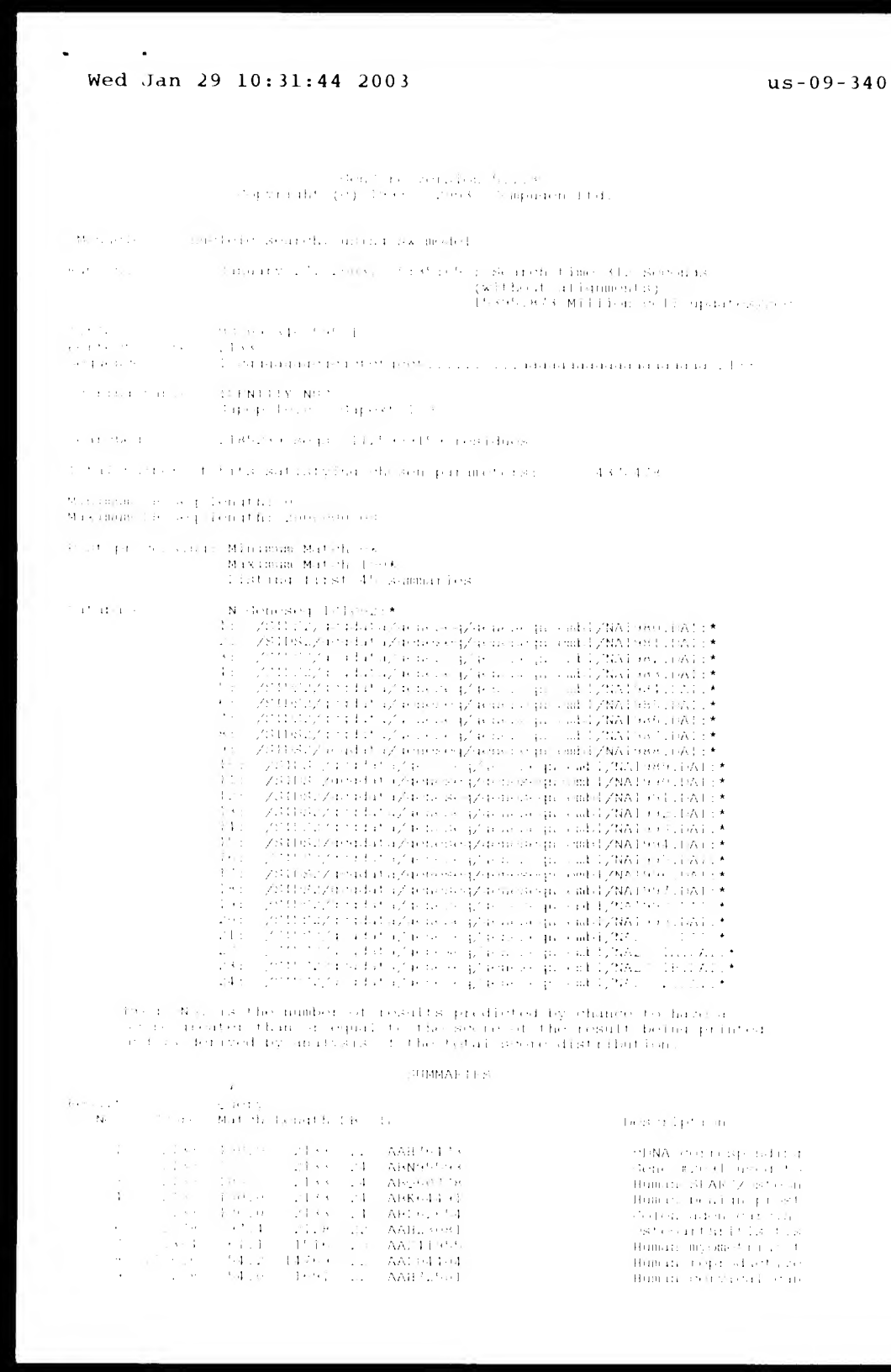

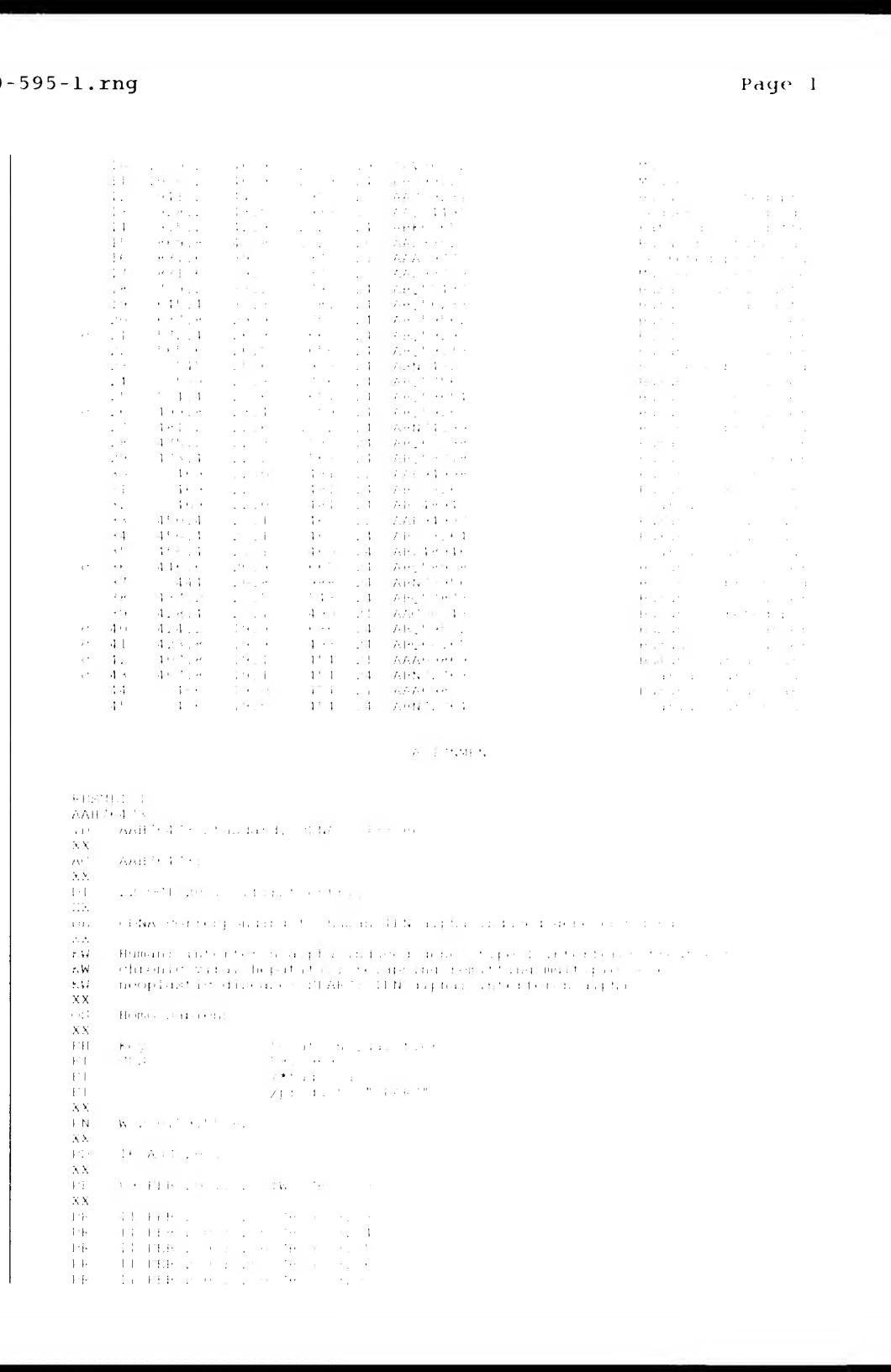

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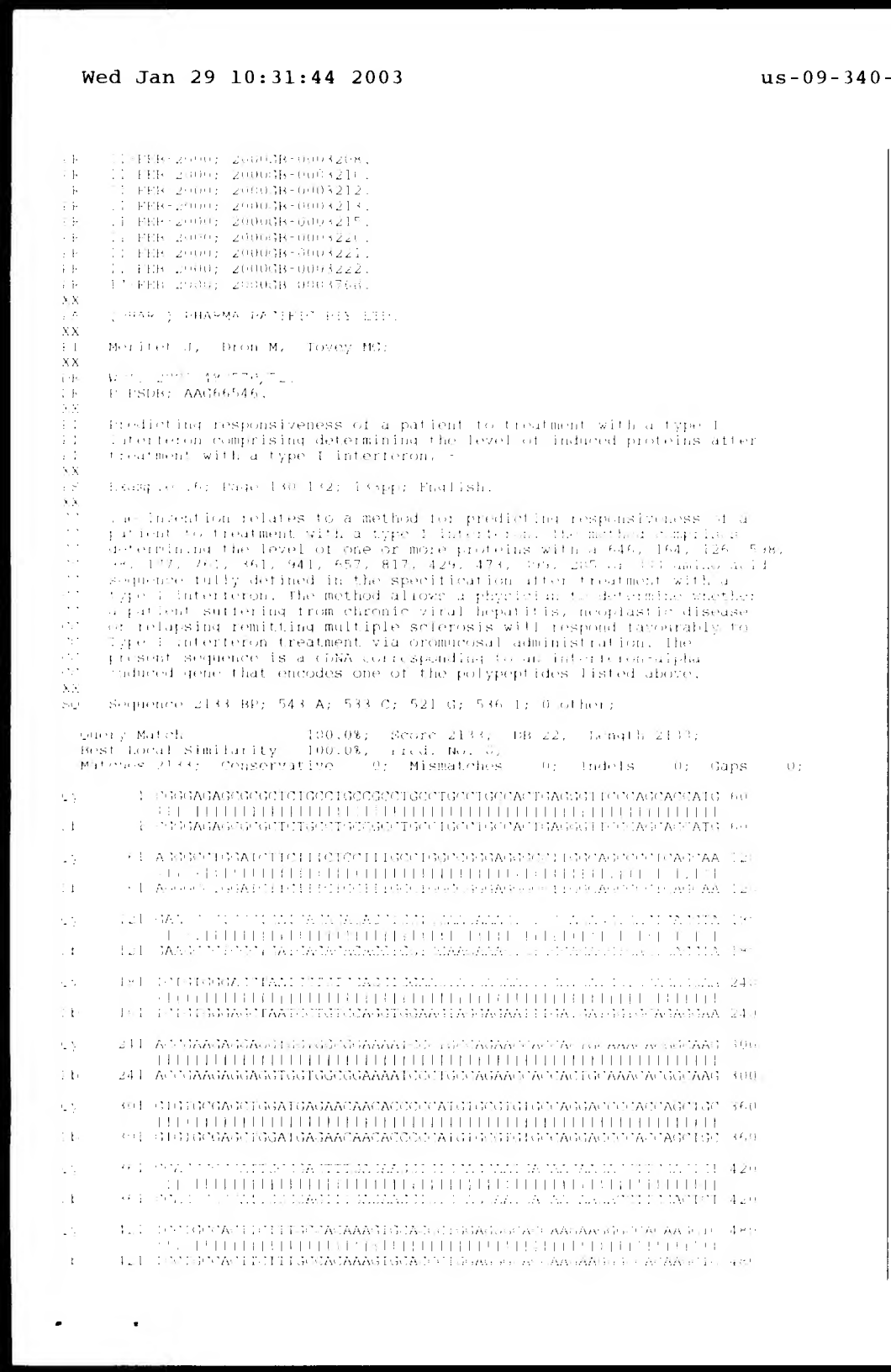
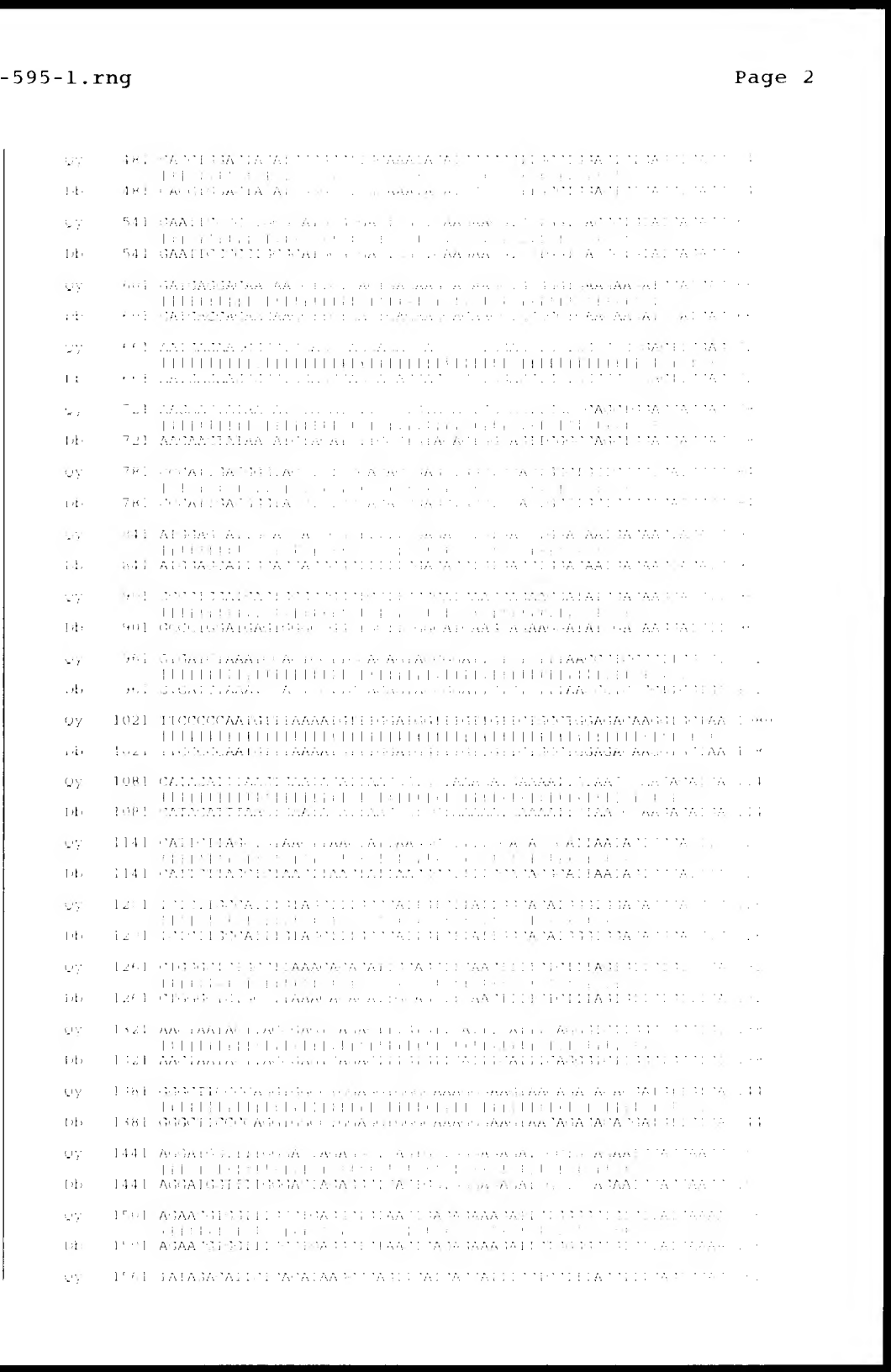
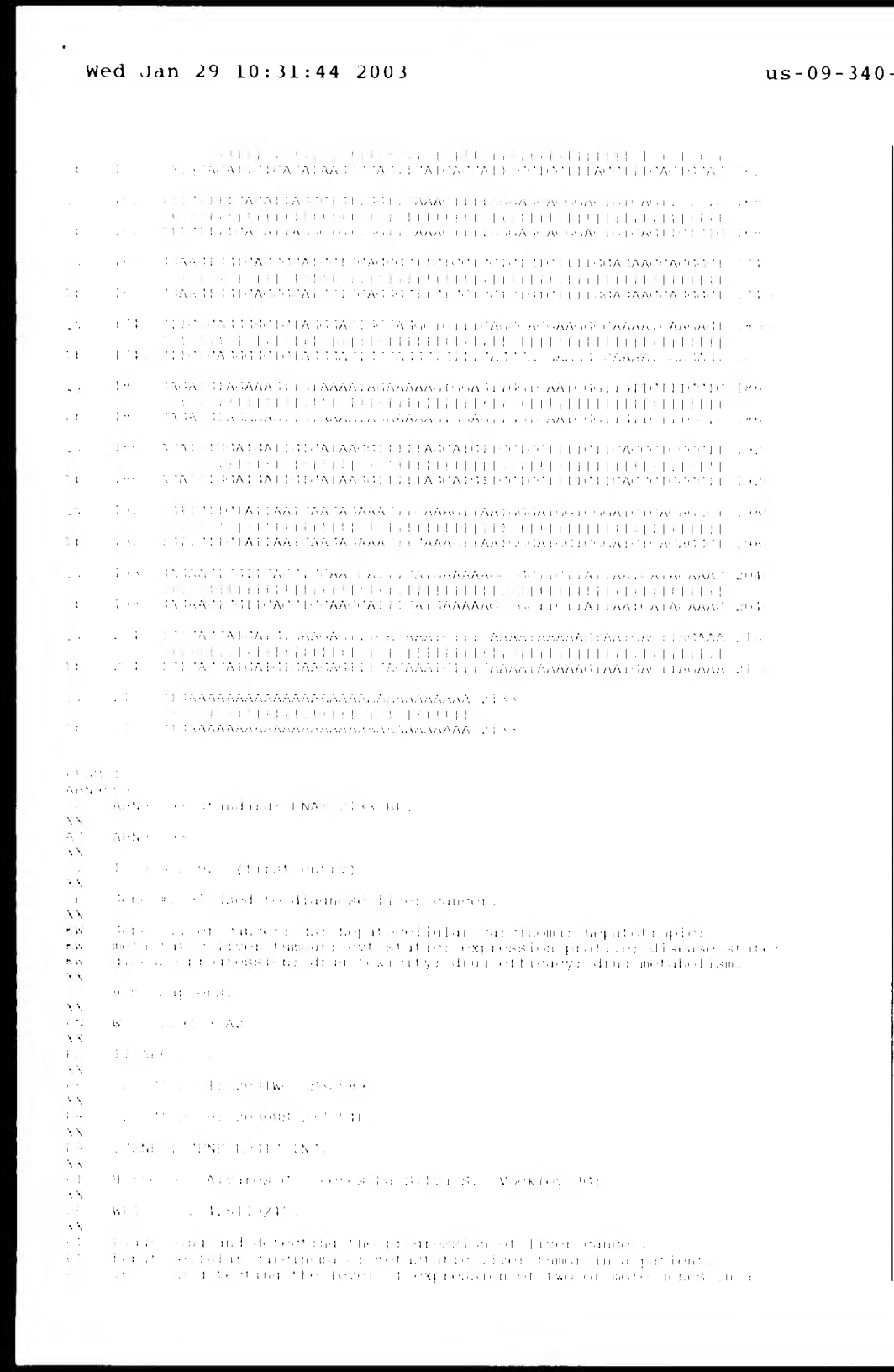
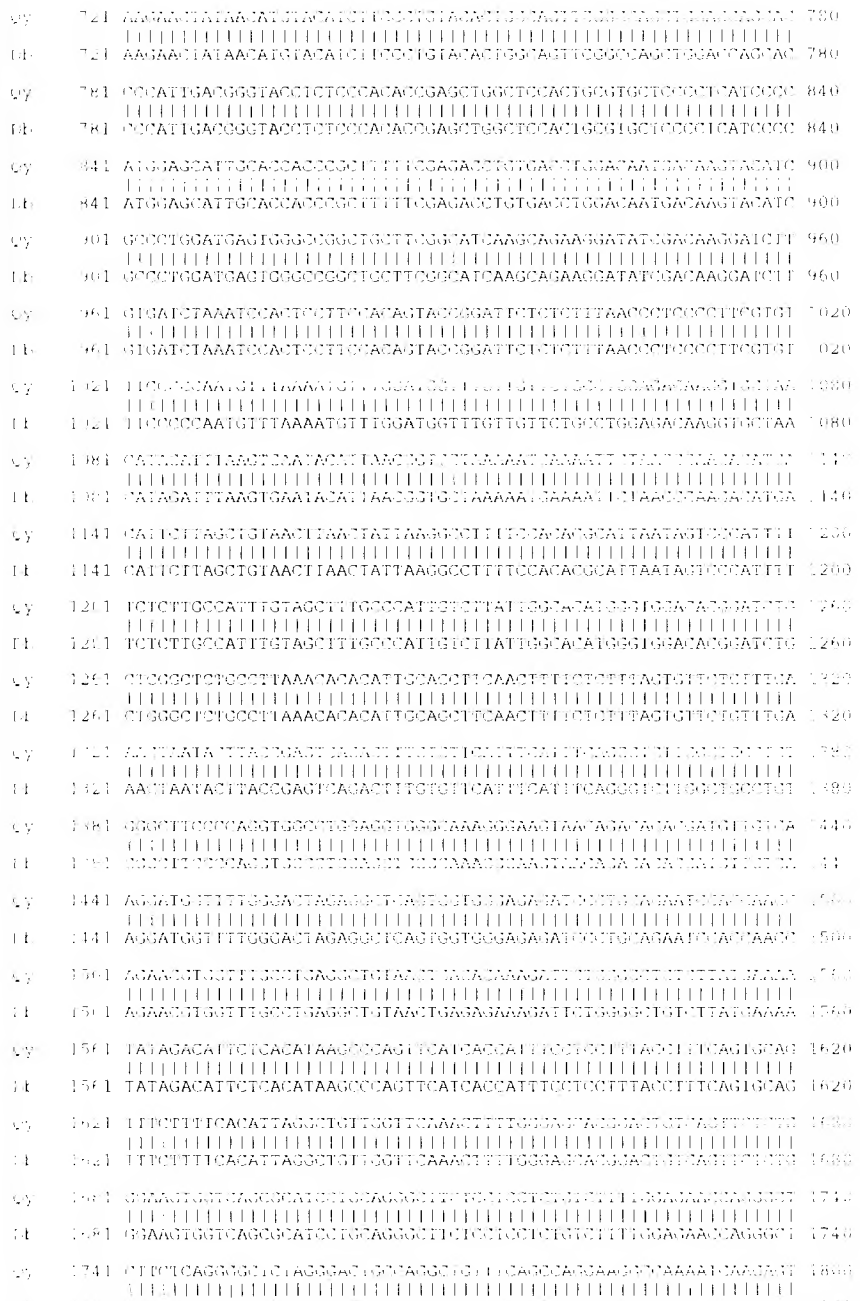
RL (in) FEB-2000; 2000GB-000328.
XX
RA (GRAY) SCHERING CORP.
XX
RT Merrill J, Dron M, Tovey MG;
XX
RL Submitted (19-FEB-2000) to EMBL.
DR PSDB; AAG66546.
XX
RT Predicting responsiveness of a patient to treatment with a type I
RT interferon comprising determining the level of induced proteins after
RT treatment with a type I interferon. -
XX
RL Example 6; Page 130 162; 159pp; English.
XX
CC The invention relates to a method for predicting responsiveness of a
CC patient to treatment with a type I interferon. The method comprises
CC determining the level of one or more proteins with a 646, 164, 126, 598,
CC 44, 177, 761, 861, 941, 657, 817, 429, 473, 95, 295 or 111 amino acid
CC sequence fully defined in the specification after treatment with a
CC type I interferon. The method allows a physician to determine whether
CC a patient suffering from chronic viral hepatitis, neoplastic disease
CC or relapsing remitting multiple sclerosis will respond favourably to
CC type I interferon treatment via oromucosal administration. The
CC present sequence is a cDNA corresponding to an interferon-alpha
CC induced gene that encodes one of the polypeptides listed above.
XX
SQ Sequence 2133 BP; 543 A; 533 C; 521 G; 536 T; 0 other;

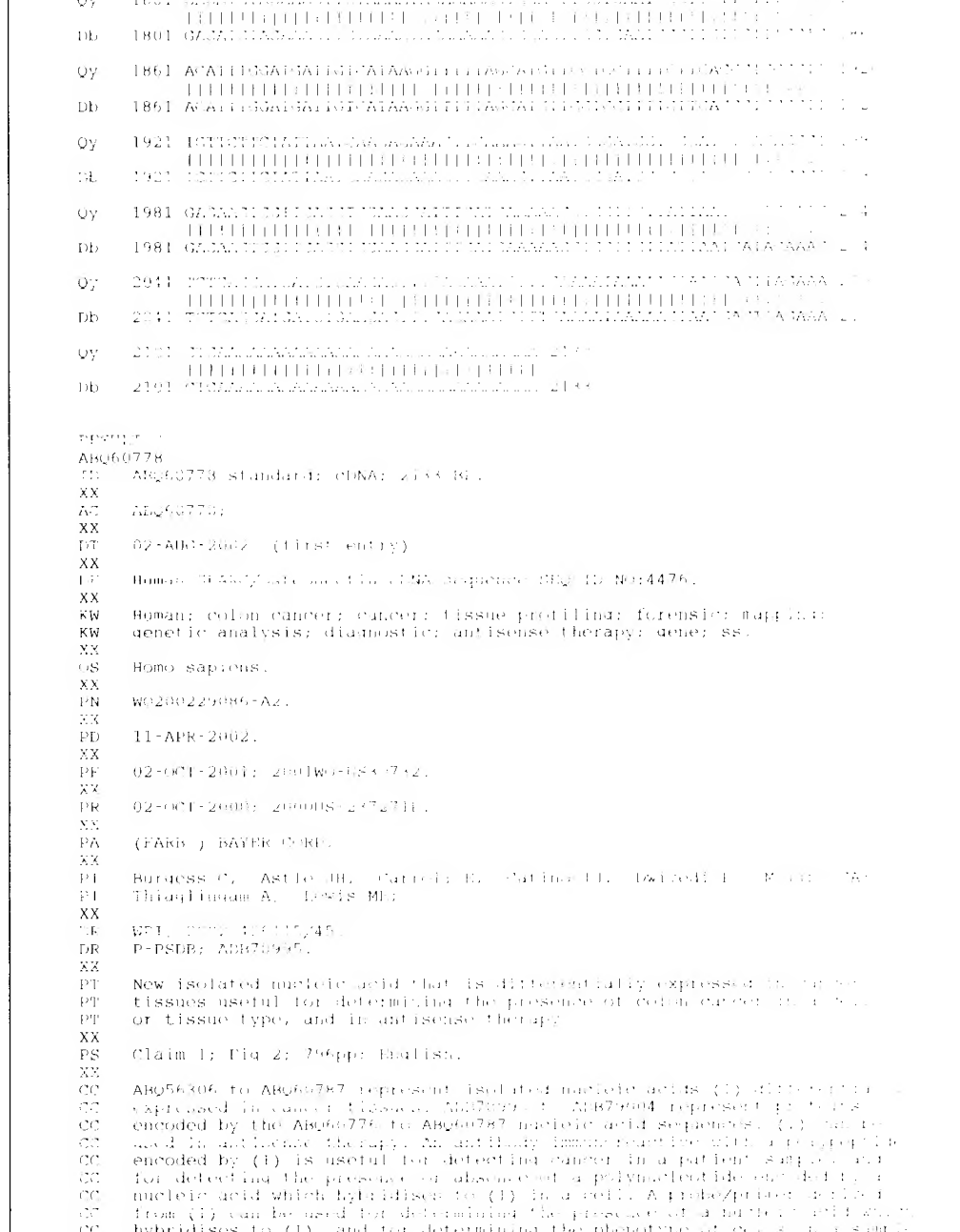
Query Match 100.0%; Score 2133; DB 22; Length 2133;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;











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XX
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XX
DT   02-AUG-2002  (first entry)
XX
DE   Human colon cancer associated cDNA sequence SEQ ID NO:4476.
XX
KW   Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW   genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200229086-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US30742.
XX
PR   02-OCT-2000; 2000US-237211.
XX
PA   (FAKb ) BAYER CORP.
XX
PI   Burgess C, Astle JM, Carroll E, Catino JJ, Dzialoski E, Mack DH,
PI   Thiagalingam A, Lewis ME;
XX
DR   WPI; 2002-[illegible]/45.
DR   P-PSDB; ADB78905.
XX
PT   New isolated nucleic acid that is differentially expressed in colon
PT   tissues useful for determining the presence of colon cancer in a cell
PT   or tissue type, and in antisense therapy
XX
PS   Claim 1; Fig 2; 796pp; English.
XX
CC   ABQ56306 to ABQ60787 represent isolated nucleic acids (1) differentially
CC   expressed in cancer tissues. ADB78904 - ADB79604 represent proteins
CC   encoded by the ABQ60778 to ABQ60787 nucleic acid sequences. (2) useful
CC   used in antisense therapy. An antibody immunospecific with a polypeptide
CC   encoded by (1) is useful for detecting cancer in a patient sample, and
CC   for detecting the presence or absence of a polynucleotide or [illegible]
CC   nucleic acid which hybridises to (1) in a cell. A probe/primer which is
CC   from (1) can be used for determining the presence of a nucleic acid which
CC   hybridises to (1), and for determining the phenotype of cells in a sample
CC   of cells from a patient. (1) is useful for determining the presence of
CC   colon cancer in a cell or tissue type, for determining the presence
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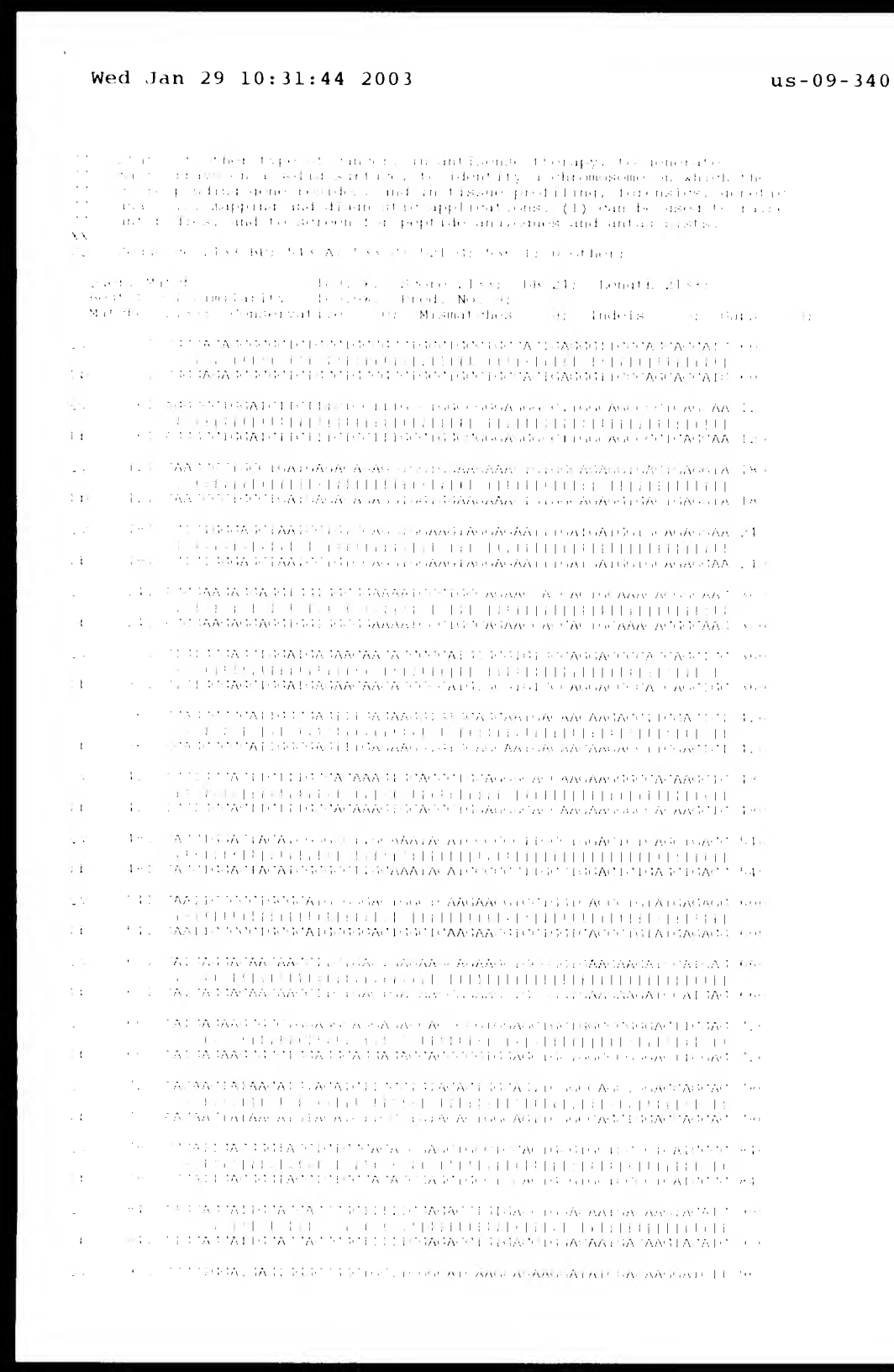

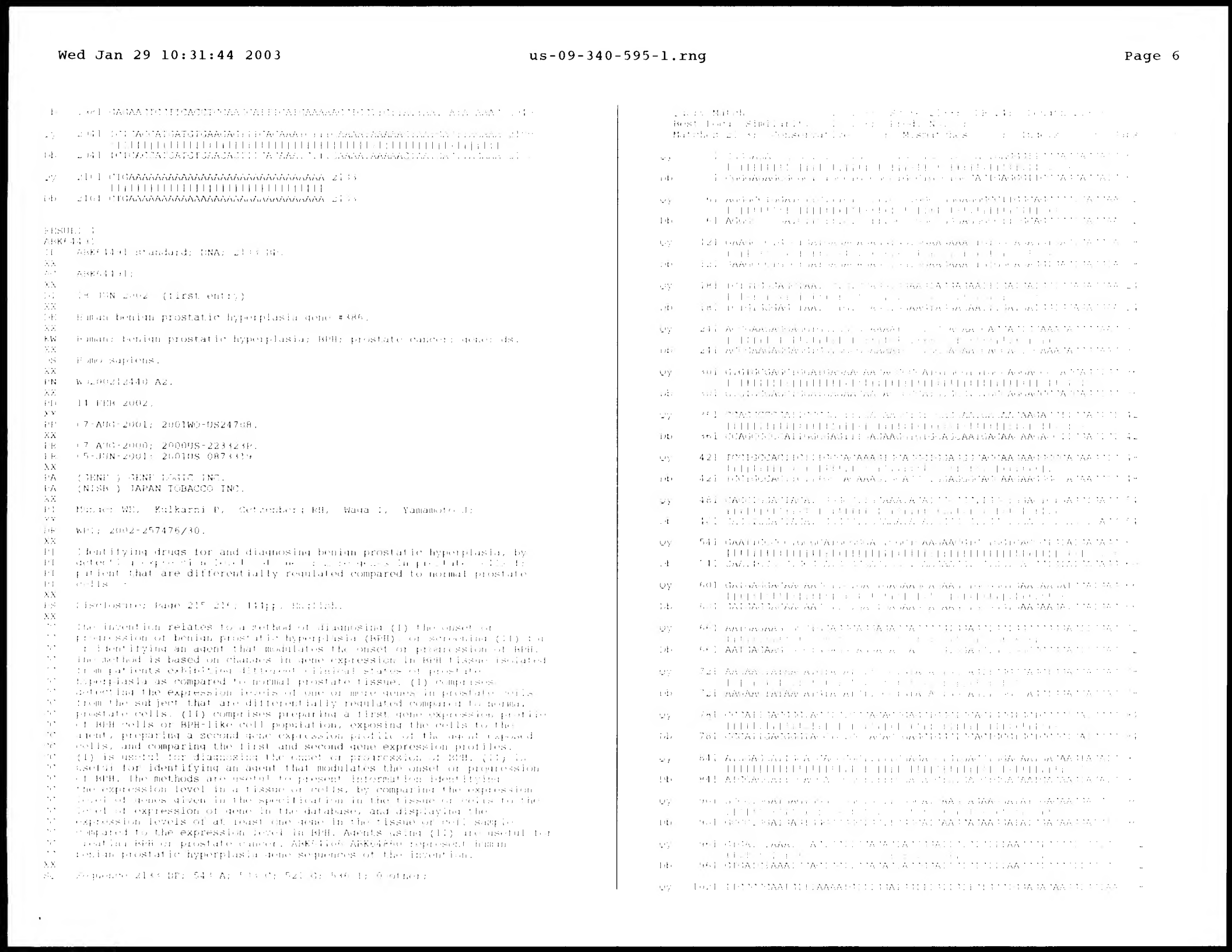

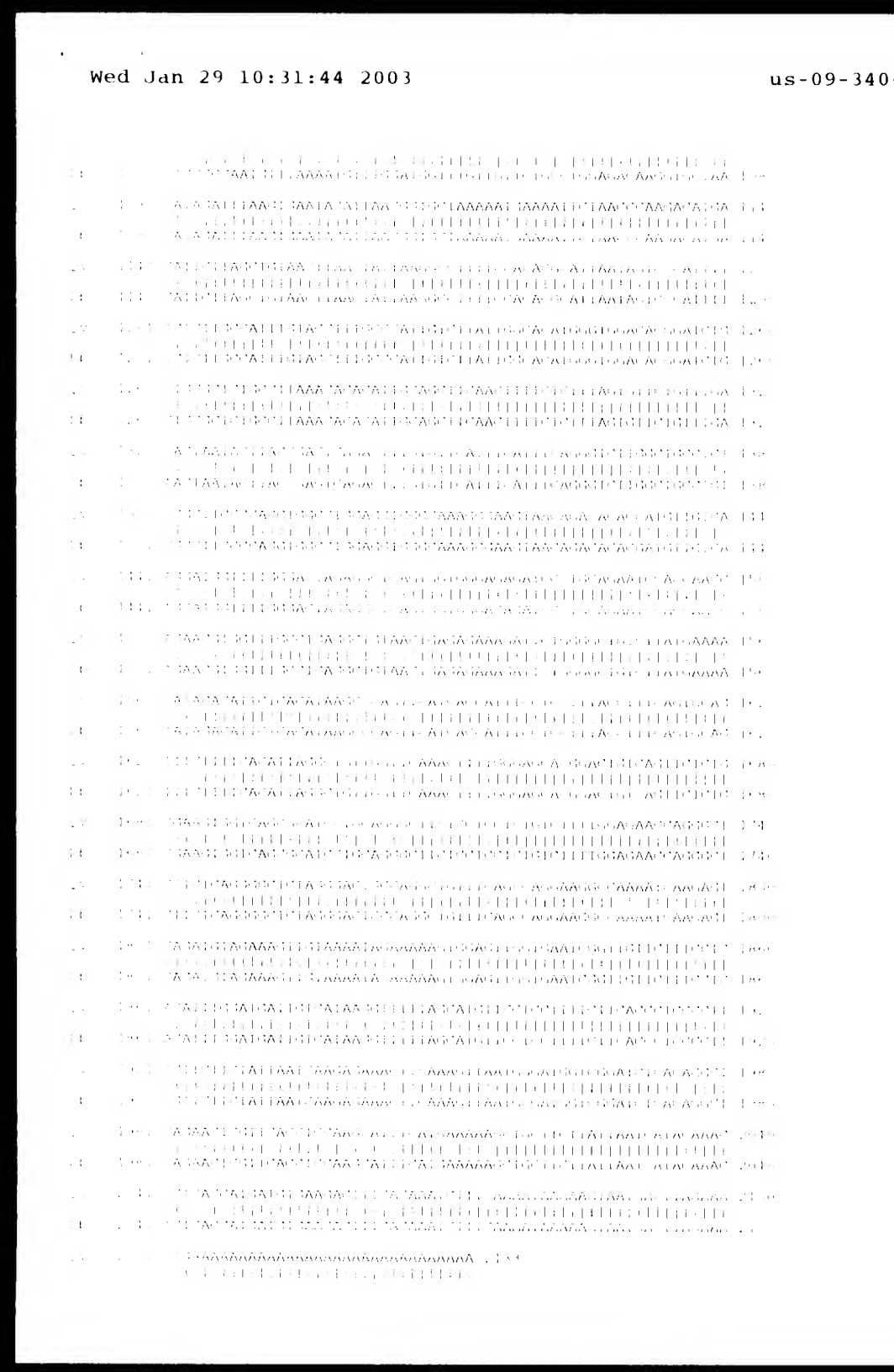

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XX
DE   WO, 2002 100264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a
PT   chemical agent to be tested for anti-neoplastic activity, and
PT   determining a change in expression of a gene of a signature gene set -
XX
PS   Claim 1; SEQ ID 991; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an
CC   anti-neoplastic agent. The method involves exposing cells to a chemical
CC   agent to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences given in ABL21664
CC   to ABL29110; (S) is at least 75% identical to (X), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for: screening
CC   an anti-neoplastic agent, and can be used for producing a product which
CC   is the data collected with respect to the anti-neoplastic agent as a
CC   result of M1, and the data is sufficient to convey the chemical
CC   structure and/or properties of the agent. M1 can be used in the
CC   treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC   oesophageal, ovarian, kidney, prostate or pancreatic cancer
CC   adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC   infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC   carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ   Sequence 2133 BP; 543 A; 533 C; 521 G; 536 T; 0 other;

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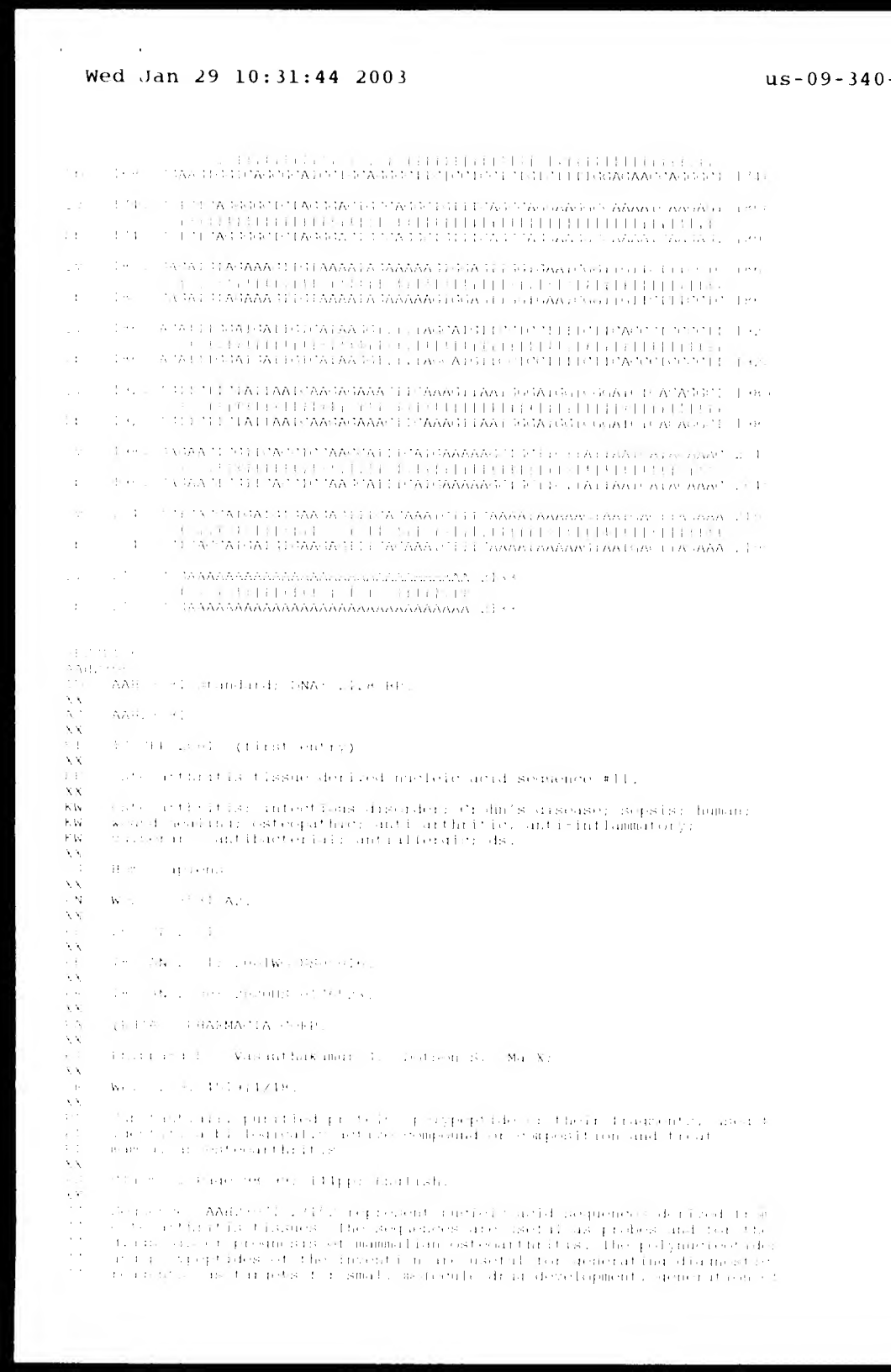

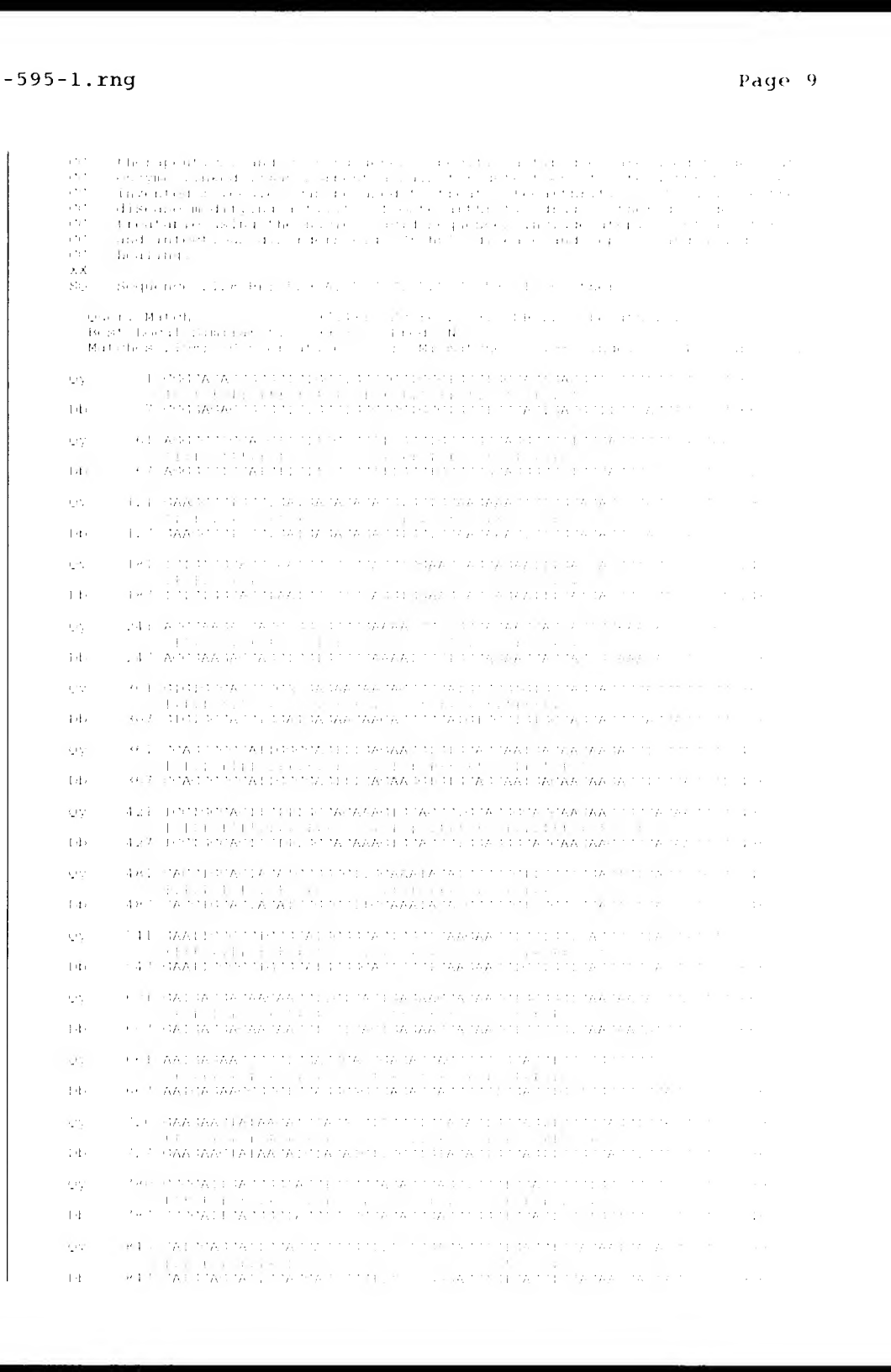

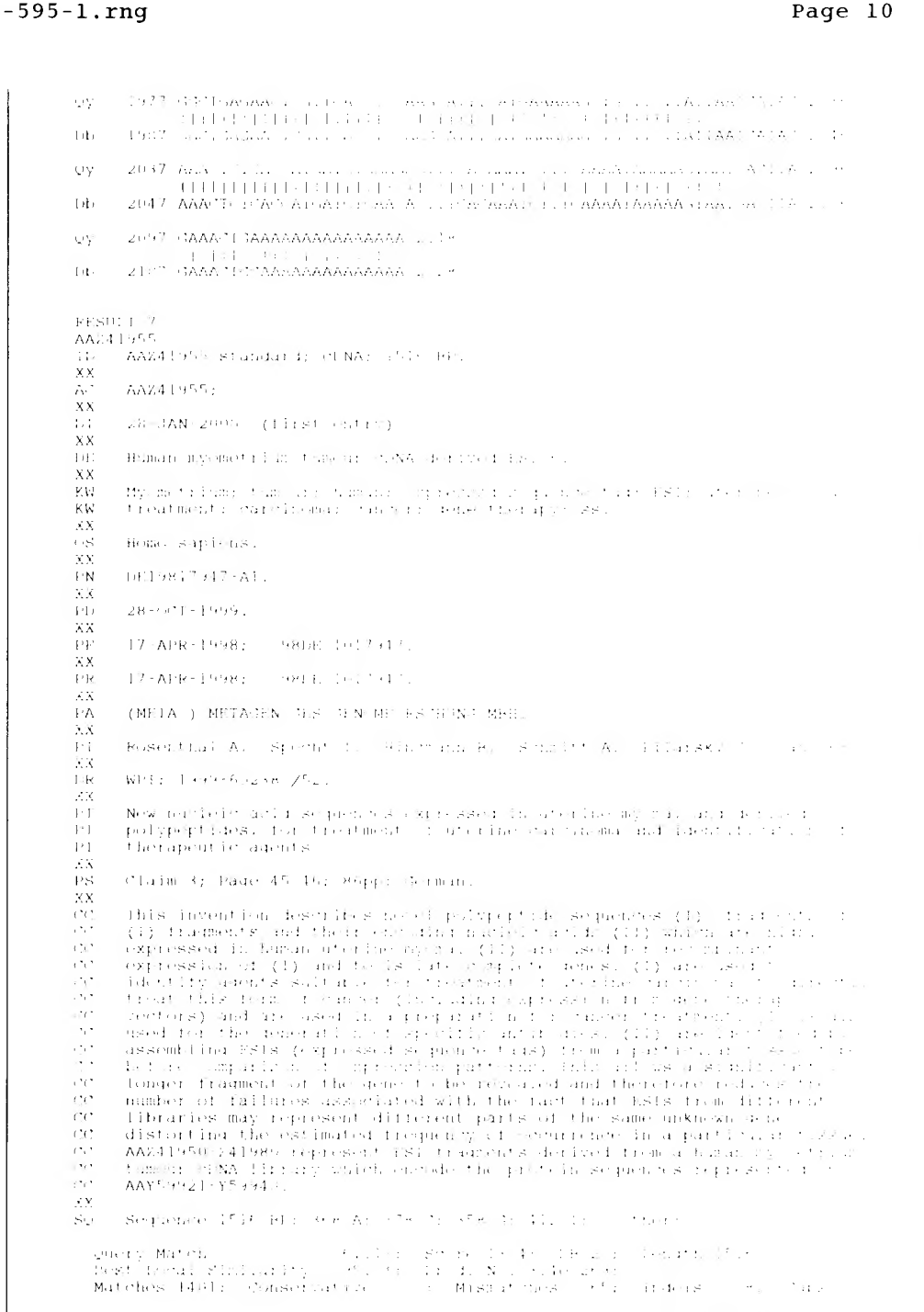

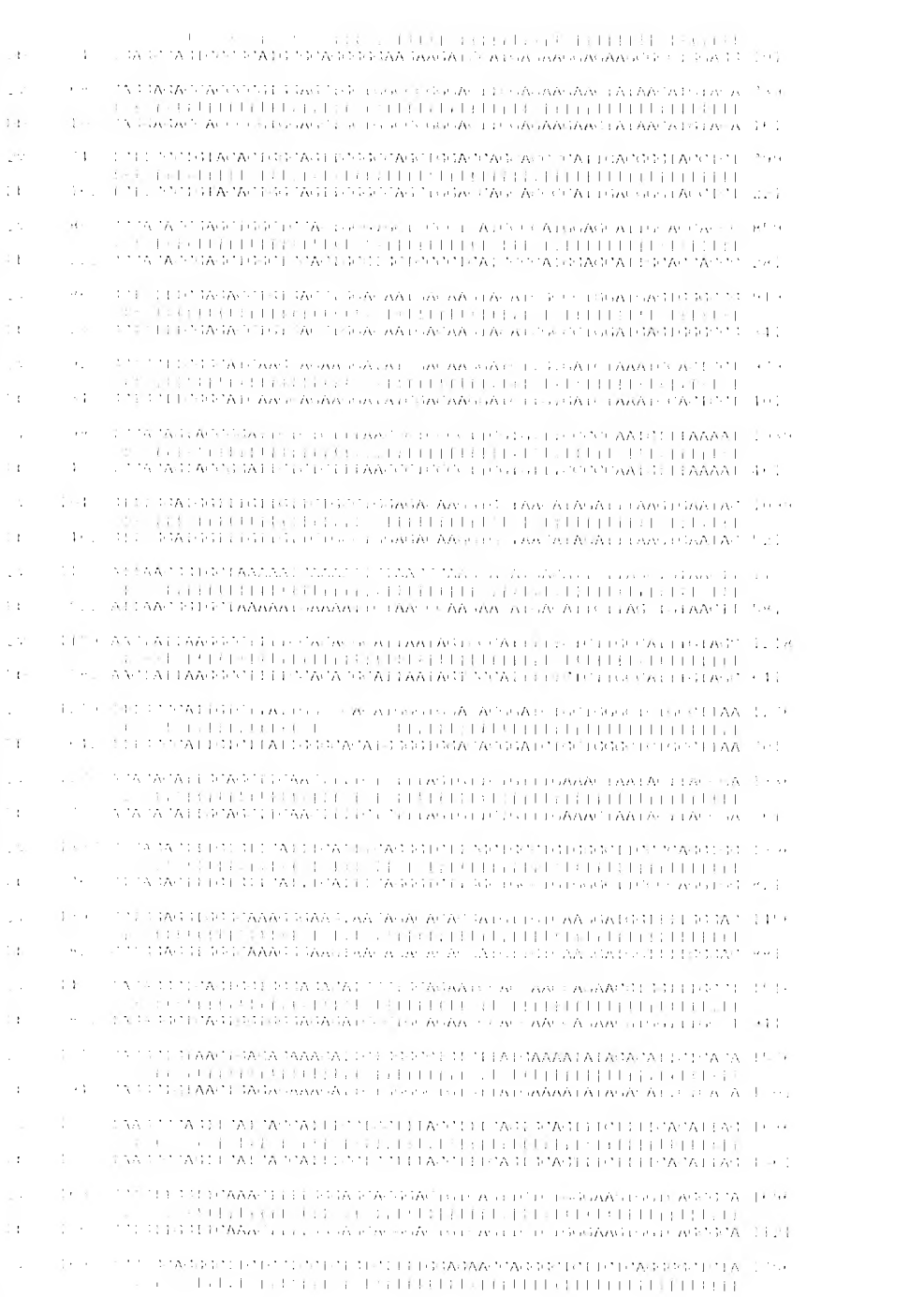

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PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Ruben SM, [illegible] SM;
XX
DR   WPI; 200[illegible], [illegible]/5[illegible].
XX
PT   Isolated nucleic acid molecule encoding a reproductive system [illegible]
PT   is used in preventing, treating or ameliorating a medical [illegible]
XX
PS   Disclosure; SEQ ID NO [illegible]; [illegible]pp; [illegible] Sequence Listing; [illegible]
XX
CC   The present invention provides the protein and coding sequence [illegible]
CC   number of human reproductive system related antigens. [illegible]
CC   in the prevention and treatment of reproductive system disorders
CC   including cancer. The present sequence is a genomic sequence [illegible]
CC   protein of the invention.
XX
SQ   Sequence [illegible] BP; [illegible]

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                 [illegible]
Db   12611 A[illegible]
 
Qy    1001 [illegible]AAAA[illegible]
                 [illegible]
Db   12674 [illegible]AA[illegible]AAAA[illegible]

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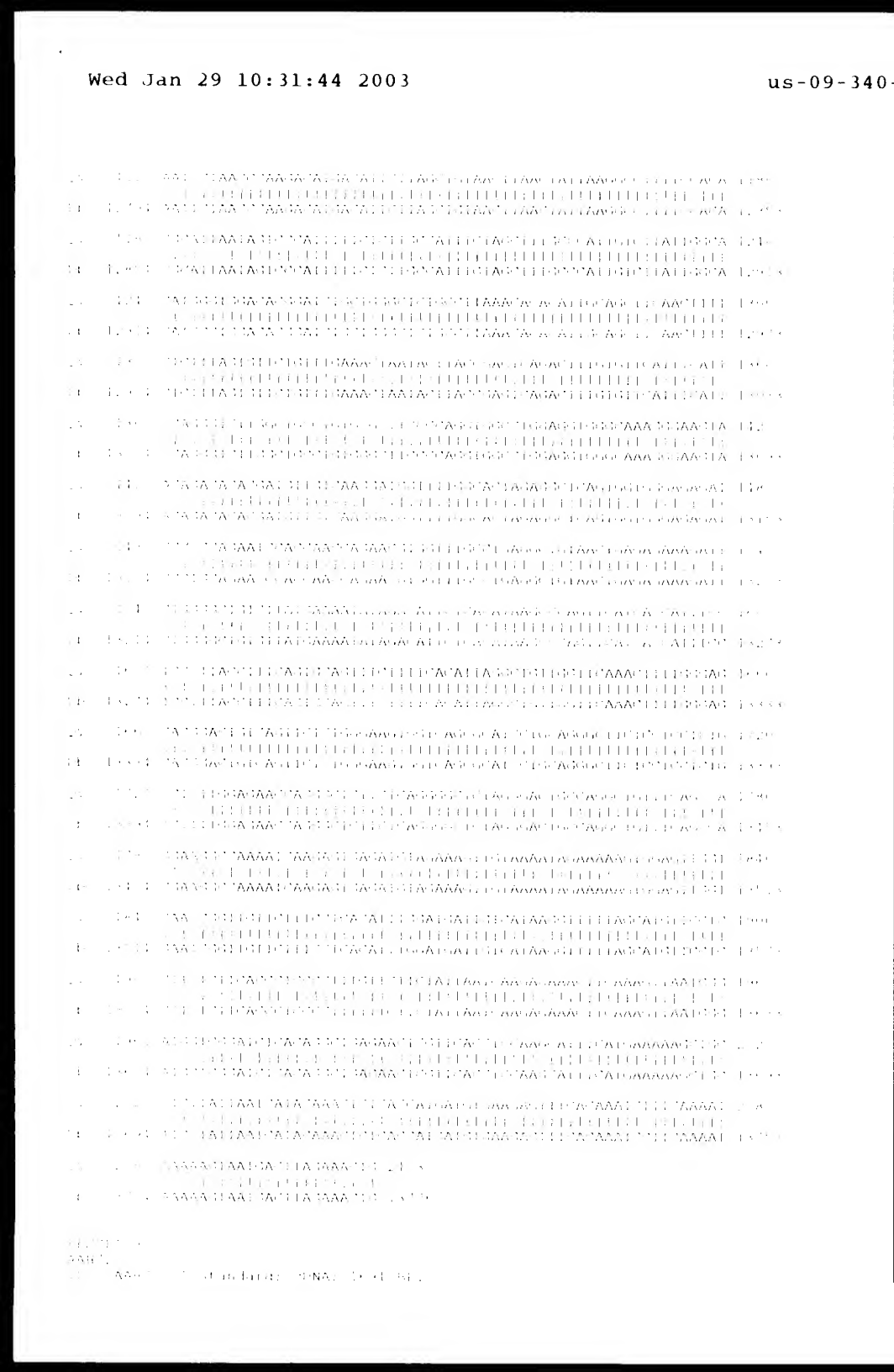

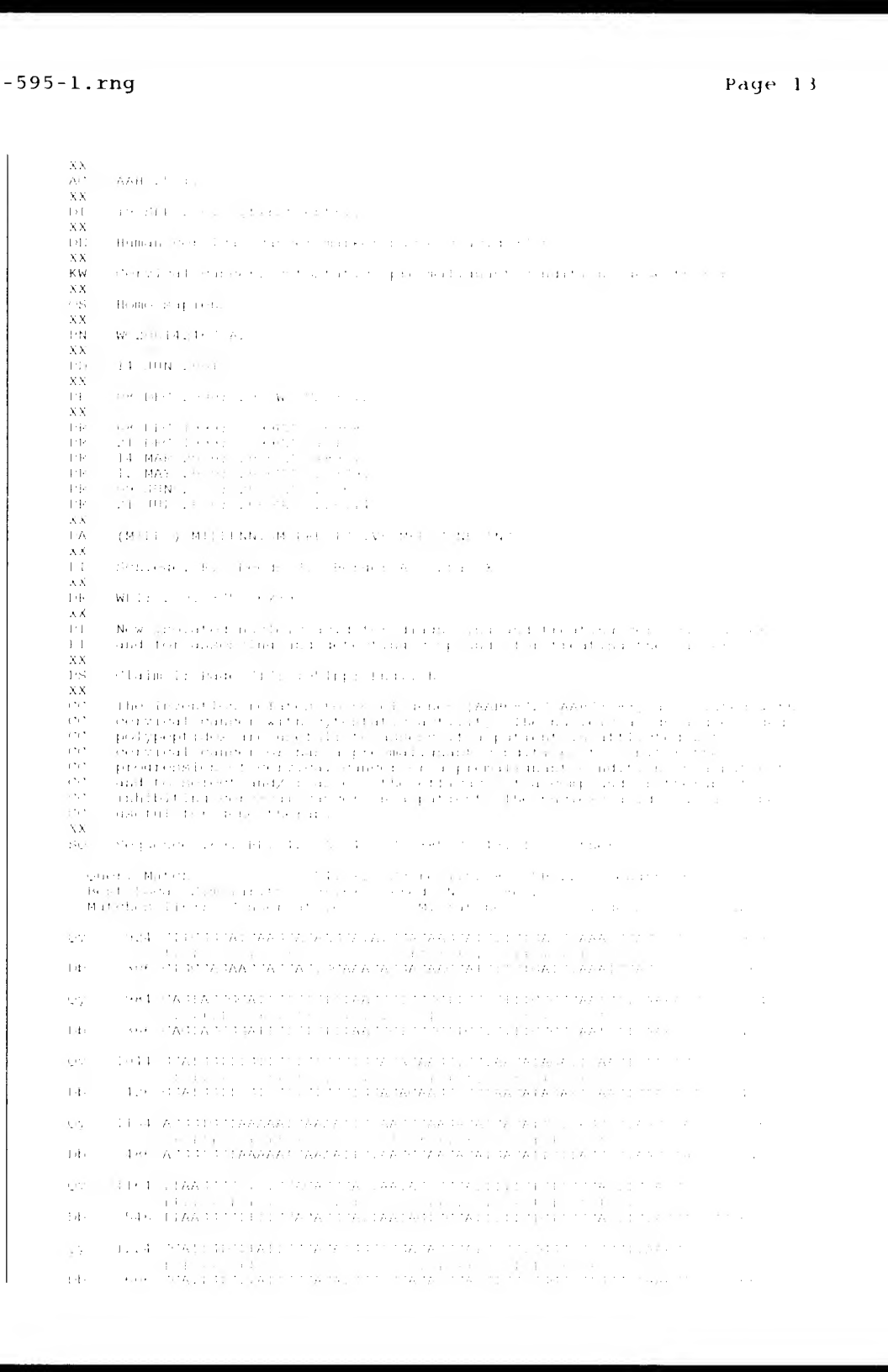

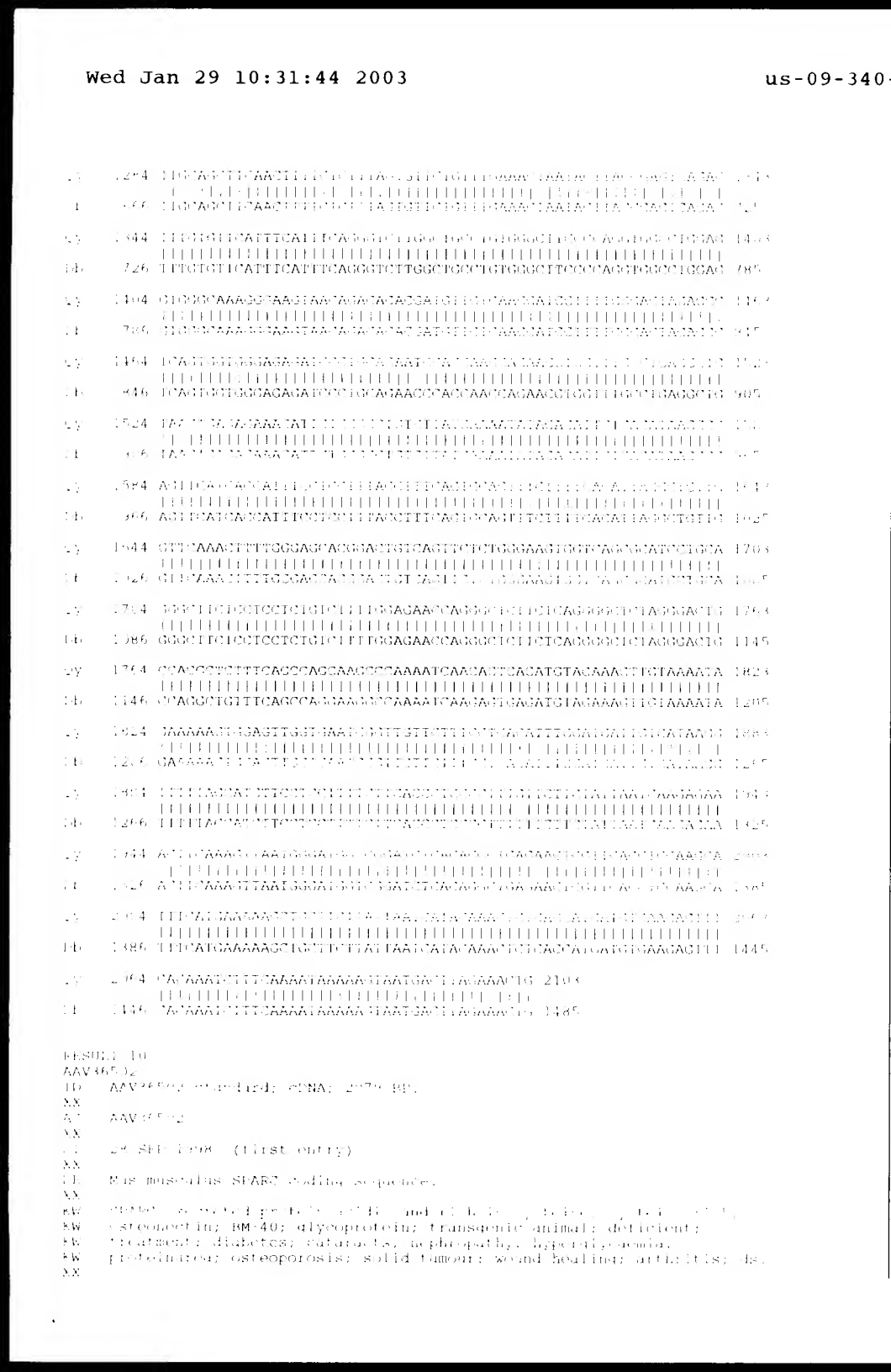

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XX
AC AAV36502;
XX
DT 29-SEP-1998 (first entry)
XX
DE Mus musculus SPARC coding sequence.
XX
KW osteonectin; BM-40; glycoprotein; transgenic animal; deficient;
KW treatment; diabetes; cataracts; nephropathy; hyperglycaemia;
KW prednisone; osteoporosis; solid tumour; wound healing; arthritis; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT misc_feature
FT /*tag= a
FT /note= "SPARC"
FT polyA_signal
FT /*tag= b
XX
PN WO9822132-A1.
XX
PD 11-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US020172.
XX
PR 07-NOV-1996; 96US-0030172.
XX
PA (WEST) WESTAB INST ANALYTICAL & PHARM.
XX
PI
XX
DR WPI; 1998-296726/26.
XX
PT New SPARC deficient transgenic mammals - useful in drug, e.g. for
PT products for treating disorders such as diabetes, cataracts,
PT nephropathy, hyperglycaemia, predisposed to osteoporosis
XX
PS Disclosure; Page 90; 61pp; English.
XX
CC The sequence is that encoding mouse SPARC (secreted protein acidic
CC and rich in cysteine) which can be used in the production of a
CC transgenic non-human animal having a phenotype characterised by
CC the absence of SPARC otherwise endogenous to the mammal. Such
CC transgenic animals can be used to study diabetes-related conditions,
CC conditions associated with over-expression of corticosteroids, and
CC research related to solid tumour growth. They can be used in methods
CC for compounds with the ability to promote or retard wound healing, or
CC the ability to treat or prevent cataracts, diabetes mellitus,
CC nephropathy, hyperglycaemia, predisposition to osteoporosis. They
CC can be used to treat conditions associated with underexpression
CC of SPARC such as diabetes mellitus, osteoporosis, proliferative
CC cataracts and other unrelated conditions. They can also be used in
CC treating conditions associated with overexpression of SPARC such as
CC solid tumours and for retarding wound healing. Essential for the
CC associated with arthritis.
XX
SQ Sequence 2078 BP; 525 A; 555 C; 544 G; 454 T; 0 other;

Query Match
Best Local Similarity
Matches 1510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

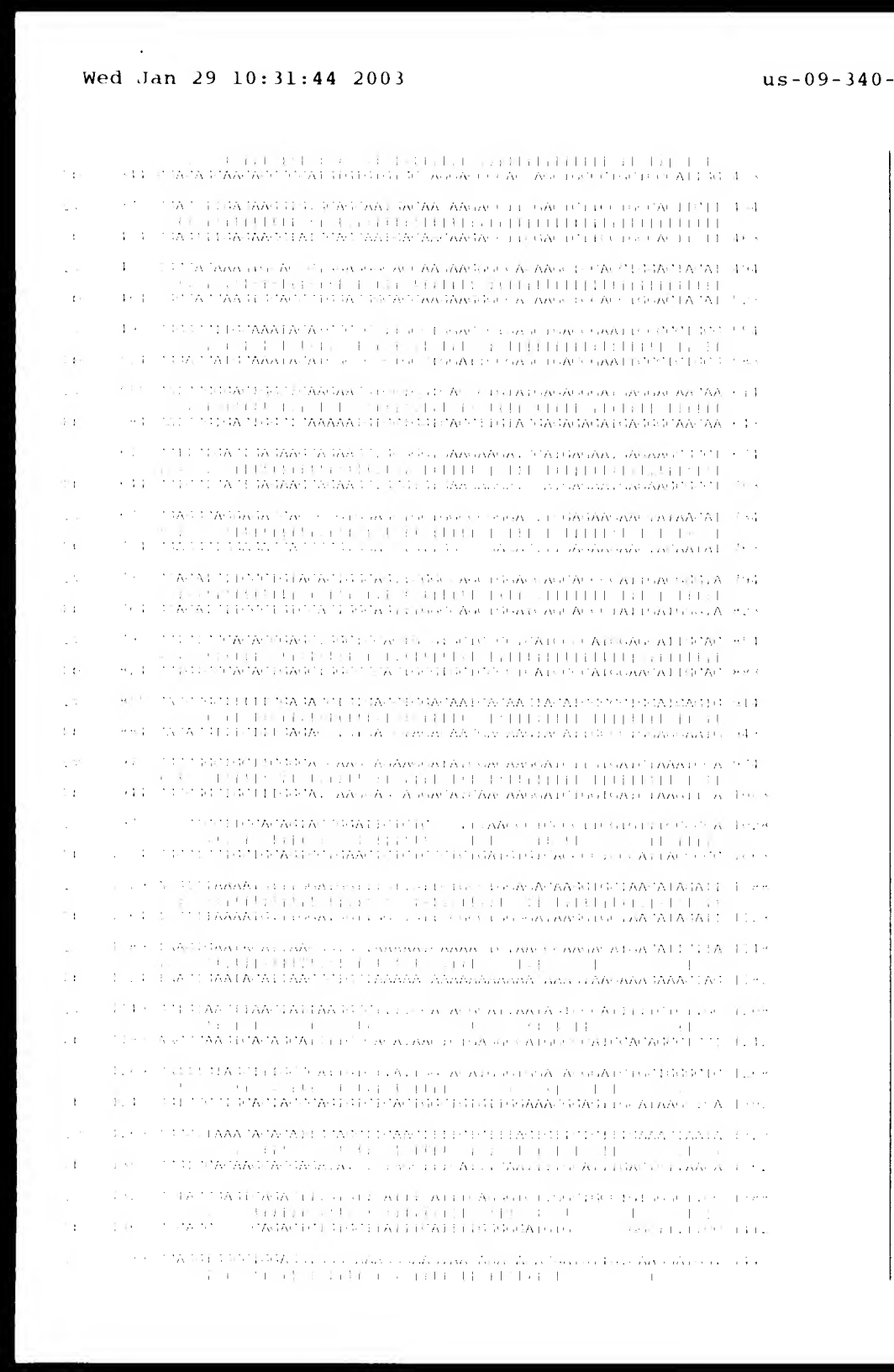
Qy
Db

Qy
Db

Qy
Db

Qy
Db

Qy
Db



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PA   ([illegible]) UNIV NIHON [illegible].
XX
PI   Ishikawa K, [illegible]
XX
DR   WO[illegible]
DR   P-PSDB; ABB57028.
XX
PT   Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT   expression levels of particular genes defined in the specification or
PT   by determining the expression profile of a gene group comprising these
PT   genes -
XX
PS   Claim 2; Page 108 110; 2[illegible]pp; English.
XX
CC   The present invention describes a method for examining ischaemic
CC   conditions, comprising measuring the expression levels of particular
CC   genes (I) in a test sample or determining the expression profile of a
CC   gene group in the sample comprising genes selected from (I). The method
CC   is useful for examining the ischaemic condition (e.g. [illegible]
CC   ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC   expression levels of particular genes (AB199202 to AB199912, encoding
CC   the protein sequences in ABB57028 to ABB57374) or by determining the
CC   expression profile of a gene group comprising these genes. The
CC   expression levels or expression profiles produced by these genes are
CC   used as an indicator when screening for ischaemic condition improving
CC   drugs or therapeutics for ischaemic diseases. AB199913 and AB199914
CC   represent PCR primers for a mouse ischaemic condition related sequence,
CC   which are used in the exemplification of the present invention.
XX
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Qy       75 [illegible] 134

Db      107 [illegible] 166

Qy      135 [illegible] 194

Db      167 [illegible] 223

Qy      195 [illegible] 254

Db      224 [illegible] 283

Qy      255 [illegible] 314

Db      284 [illegible] 343

Qy      315 [illegible] 374

Db      344 [illegible] 403

Qy      375 [illegible] 434

Db      404 [illegible] 463

Qy      435 [illegible] 494

Db      464 [illegible] 523

Qy      495 [illegible] 554

Db      524 [illegible] 583

Qy      555 [illegible] 614

Db      604 [illegible]

Qy      [illegible]

Db      641 [illegible]

Qy      675 [illegible]

Db      701 [illegible]

Qy      735 [illegible]

Db      764 [illegible]

Qy      795 [illegible]

Db      824 [illegible]

Qy      855 [illegible]

Db      881 [illegible]

Qy      915 [illegible]

Db      944 [illegible]

Qy      970 [illegible]

Db     1004 [illegible]

Qy     1029 [illegible]

Db     1064 [illegible]

Qy     1089 [illegible]

Db     1124 [illegible]

Qy     1149 [illegible]

Db     1183 [illegible]

Qy     1209 [illegible]

Db     1243 [illegible]

Qy     1269 [illegible]

Db     1303 [illegible]

Qy     1329 [illegible]

Db     1363 [illegible]

Qy     1389 [illegible]

Db     1413 [illegible]

Qy     1449 [illegible]

Db     1465 [illegible]

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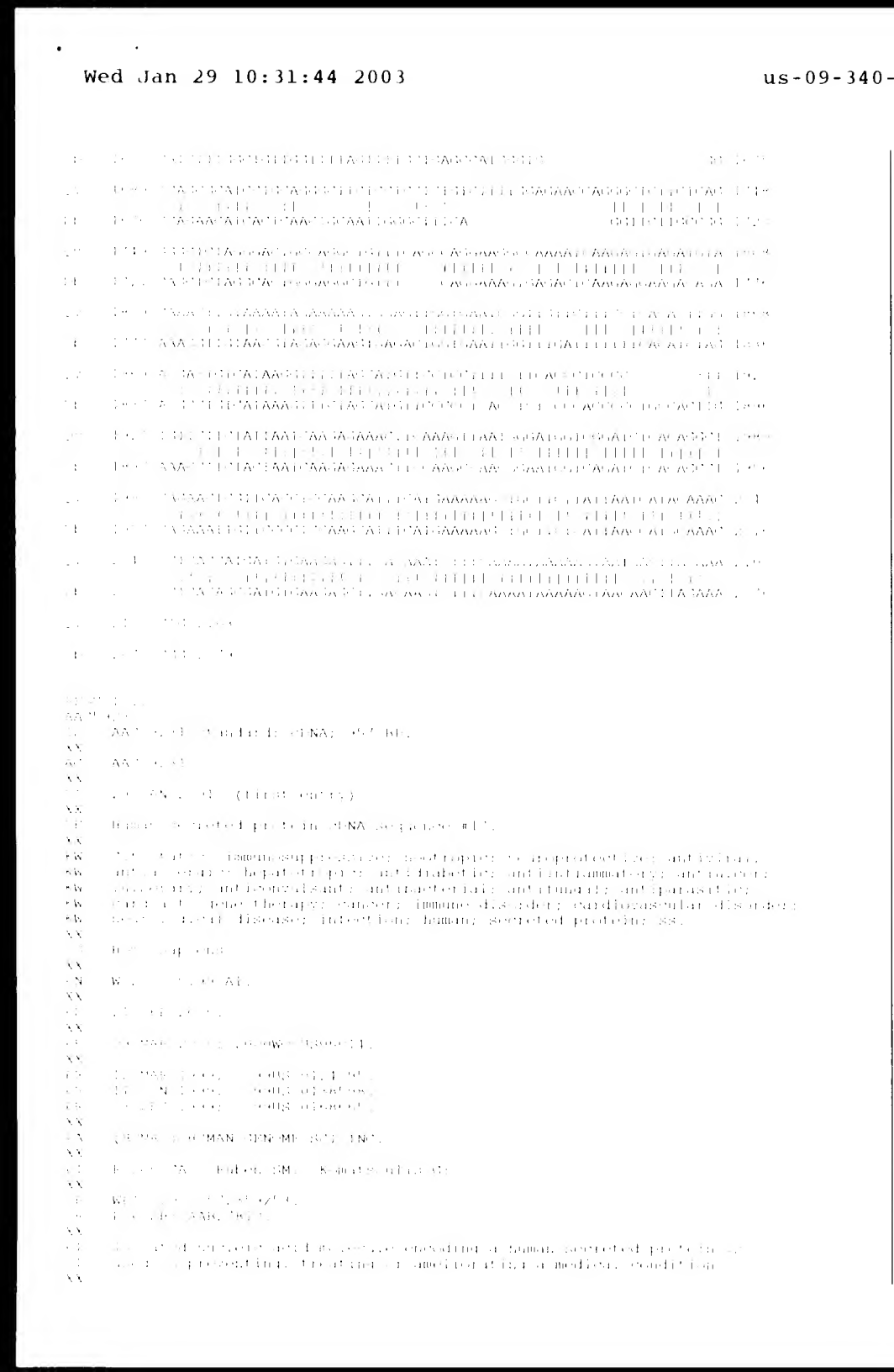

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Qy       1883 GTTTTTAGCATGTTCCTCCTTTTCTTCACCCTCCCTTTGTTCTTCTATTAATCAAGAGA 1942
              ||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||||
Db        724 GTTTTTAGCATGTTCCTCCTTTTCTTCACCCTCCCTTTGGCTTCTATTAATCAAGAGA 783

Qy       1943 AACTTCAAAGTTAATGGGATGGTCGGATCTCACAGGCTGAGAACTCGTTCACCTCCAAGC 2002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AACTTCAAAGTTAATGGGATGGTCGGATCTCACAGGCTGAGAACTCGTTCACCTCCAAGC 843

Qy       2003 ATTTCATGAAAAAGCTGCTTCTTATTAATCATACAAACTCTCACCATGATGTGAAGAGTT 2062
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Qy       2063 TCACAAATCTTTCAAAATAAAAAGTAATGACTTAGAAACTGAAAAAAAAAAAAA 2116
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Db        904 TCACAAATCTTTCAAAATAAAAAGTAATGACTTAGAAAAAAAAAAAAAAAAAAA 957
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XX
AC   AAQ04435;
XX
DT   17-DEC-2001  (updated)
DT   04-OCT-1990  (first entry)
XX
DE   Sequence encoding human bone osteonectin(ON).
XX
KW   Osteoporosis; rheumatoid arthritis; Paget's disease;
KW   [illegible]
XX
OS   Homo sapiens
XX
FH   Key             Location/Qualifiers
FT   CDS             22..930
FT                   /*tag= a
XX
PN   [illegible]
XX
PD   17-AUG-1990.
XX
PF   [illegible]
XX
PR   [illegible]
XX
PA   (USSH ) NAT INST OF HEALTH.
XX
PI   Termine J;
XX
DR   WPI; 1990-[illegible]
DR   P-PSDB; AAR05164.
XX
PT   Human bone matrix DNA and proteins -
PT   used in detection, diagnosis and treatment involving skeletal
PT   and/or connective tissue disease states.
XX
PS   Disclosure; ; p; English.
XX
CC   Probes and Abs raised to the proteins can be used to determine
CC   [illegible]
CC   diseases states such as osteoporosis, osteo/rheumatoid arthritis,
CC   Paget's disease, artherosclerosis and periodontal disease.
CC   Proteins may also be used to induce or block biological function.
CC   [illegible]
CC   US Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/[illegible]
XX
SQ   Sequence 957 BP; 226 A; 2[illegible] C; 2[illegible] G; 17[illegible] T; 0 other;
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              [illegible]
Db          1 CCACTAAGG[illegible]

Qy         97 [illegible]
              [illegible]
Db         61 AGGG[illegible]

Qy        157 [illegible]
              [illegible]
Db        121 [illegible]

Qy        217 [illegible]
              [illegible]
Db        181 [illegible]

Qy        277 [illegible]
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Qy        397 [illegible]
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Qy        637 [illegible]
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              [illegible]
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Qy        757 [illegible]
              [illegible]
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Qy        817 [illegible]
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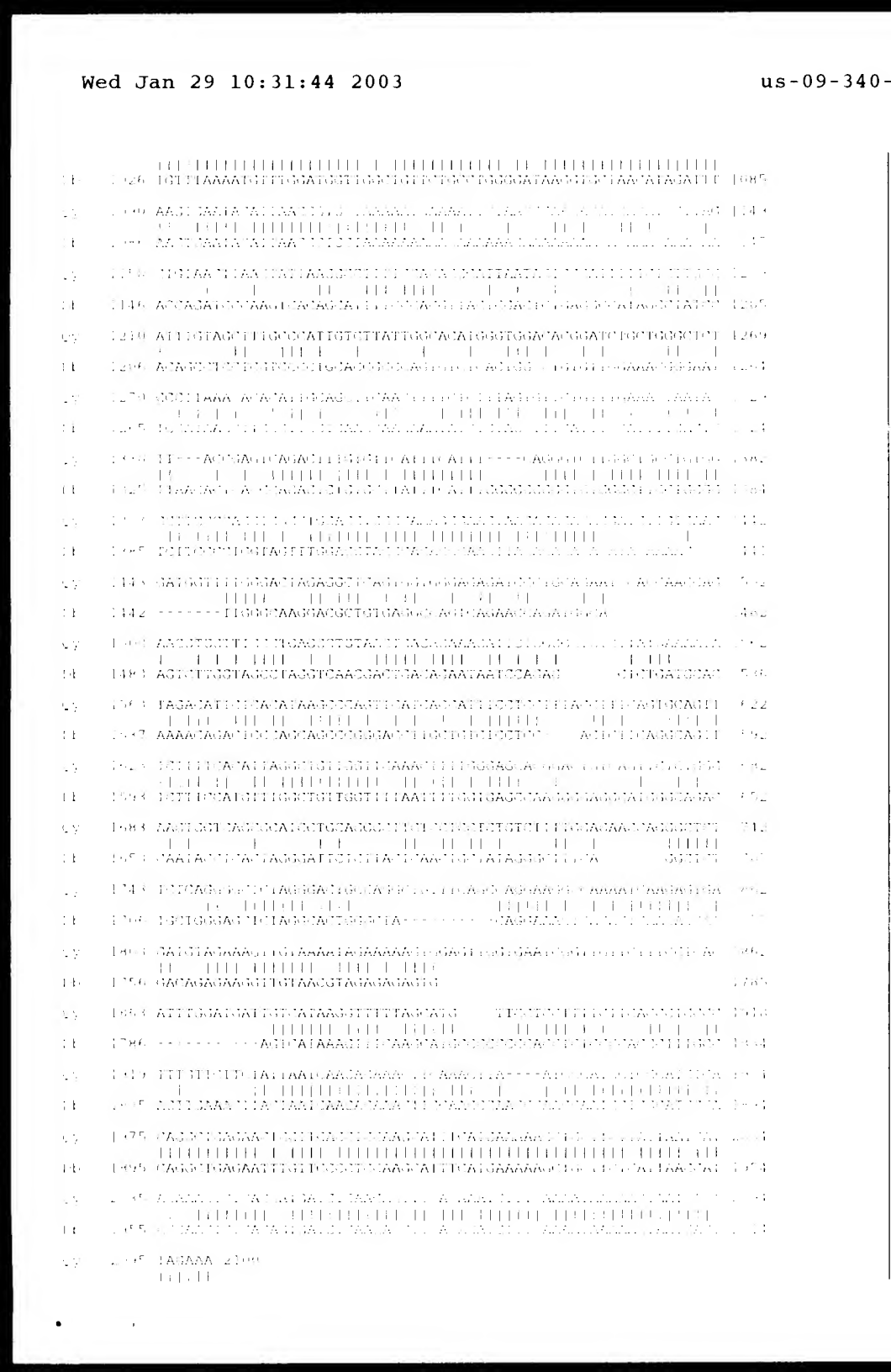

DB 2015 IAIAAA 2020

RESULT 15
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XX
AC AAZ33527;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human prostate cancer-associated EST 5'.
XX
KW Expressed sequence tag; EST; prostate cancer; breast cancer;
KW cancer tissue specificity; vaccine.
XX
OS Homo sapiens.
XX
PN DE19811194-A1.
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PD 16-SEP-1999.
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PF 10-MAR-1998; 98DE-19811194.
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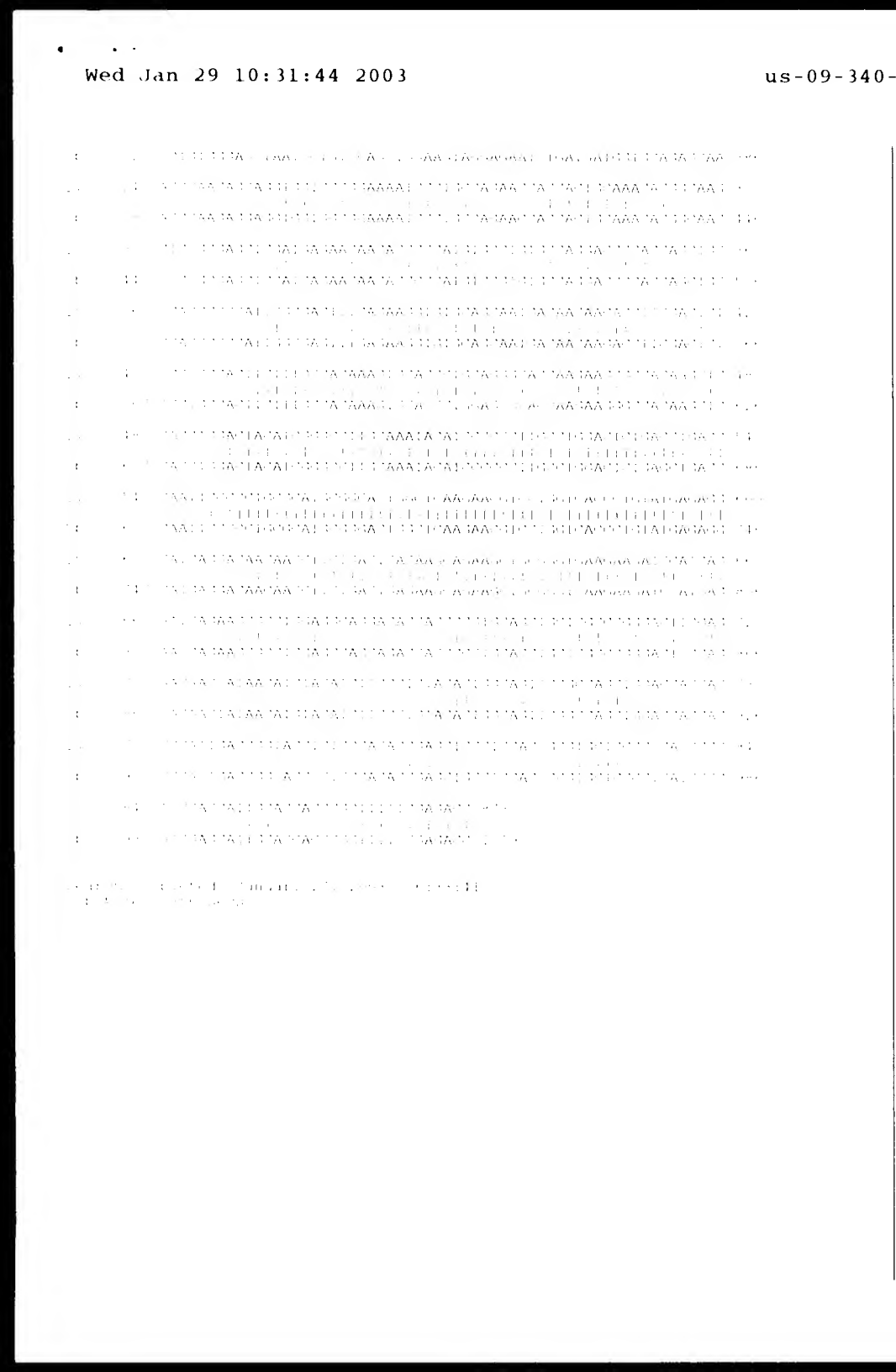
PR 10-MAR-1997; 97EP-0103911.
XX
PA (MEIA-) MEIAEN GES GEN PH GESELLSCHAFT MBH.
XX
PI Specht T, Hinzmann B, Strauss A, Lisansky T, Jahn D, Schmitz G;
XX
DR WPI; 1999-511822/44.
XX
PT New nucleic acid expressed at high level in normal prostatic tissue and
PT encoded polypeptides, used to treat cancer and screen for therapeutic
PT agents
XX
PS Claim 1; Fig 1; 61pp; German.
XX
CC This invention describes a new nucleic acid sequence (A) that is
CC expressed at high level in normal prostatic tissue, polypeptides
CC encoded by (A) are useful (a) for identifying agents for treating
CC prostatic cancer and (b) for therapy of prostate cancers. Proteins
CC where expressed by gene therapy methods. (A) is also used to isolate
CC full length genes (for gene therapy) and for recombinant production of
CC (A), which are used to raise specific antibodies. (A) is identified
CC by assembly of ESTs (expressed sequence tags) but is not limited to
CC for expression pattern (tissue specificity). This application claims
CC many of the false results, as regards tissue specificity, are likely
CC still to be worth as 'hot' candidate (usually short) ESTs. AAZ33527
CC represent expressed sequence tags described in the method of the
CC invention.
XX
SQ Sequence 1060 BP; 233 A; 256 C; 316 G; 255 T; 0 other;

Query Match 4.3%; Score 87.8; DB 20; Length
Best Local Similarity 74.0%; Pred. No. 2.9e-17;
Matches 871; Conservative 0; Mismatches 21; Gaps 1;



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	99	31.2	1.5	37	17	AI831214	AI831214	
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	102	31.2	1.5	40	12	BG166502	BG166502 602339795	
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c	104	31.2	1.5	47	10	AW250836	AW250836	
	105	31.2	1.5	48	9	AL642160	AL642160 AL642160	
	106	31.2	1.5	48	9	AL653895	AL653895 AL653895	
	107	31.2	1.5	48	9	AA852759	AA852759	
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	109	31.2	1.5	49	9	AL657892	AL657892 AL657892	
	110	31.2	1.5	50	9	AL644181	AL644181 AL644181	
	111	31	1.5	35	9	AL642929	AL642929	
	112	31	1.5	39	9	AL653882	AL653882 AL653882	
	113	31	1.5	43	9	AL636167	AL636167 AL636167	
	114	31	1.5	45	12	BG669979	BG669979 DKFZp586E12	
	115	31	1.5	46	2	HSM003158	A1038682 Homo sapi	
	116	31	1.5	49	12	BI223939	BI223939 602912861	
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	119	30.8	1.4	35	12	BE894837	BE894837 601434018	
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	121	30.8	1.4	43	9	AL636541	AL636541 AL636541	
	122	30.8	1.4	45	17	AI167957	AI167957	
	123	30.8	1.4	46	12	BG010636	BG010636 602011381	
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	127	30.6	1.4	36	2	HSM001086	A1036769 Homo sapi	
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	130	30.6	1.4	50	9	AA129846	AA129846	
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	132	30.4	1.4	34	17	AI345615	AI345615	
	133	30.4	1.4	41	2	HSM001284	A1036963 Homo sapi	
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	136	30.4	1.4	50	10	AV367273	AV367273 AV367273	
c	137	30.2	1.4	35	17	AI623128	AI623128	
c	138	30.2	1.4	37	17	AI803371	AI803371	
	139	30.2	1.4	38	2	HSM001716	A1026993 Homo sapi	
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	146	30	1.4	28	2	HSM001126	A1036658 Homo sapi	
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	189	30	1.4	48	9	BG [illegible]	[illegible]	
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	217	29.2	1.4	34	2	HSM [illegible]	[illegible]	
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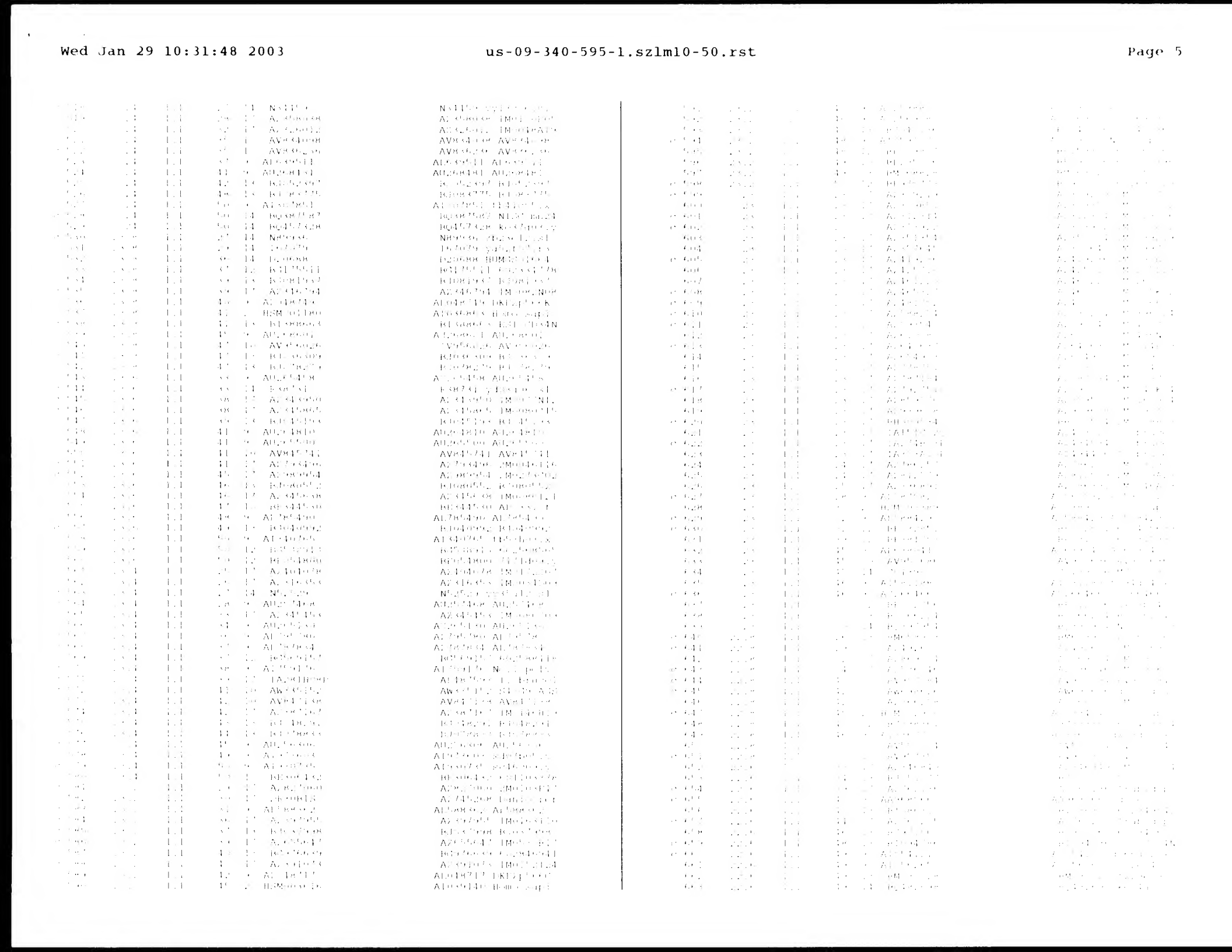

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c	672	22.4	1.1	26	14	P26779	P26779
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c	674	22.4	1.1	29	17	TA378827	AR137521
c	675	22.4	1.1	33	17	AR774479	AR774479
	676	22.4	1.1	36	10	AW059764	AW059764
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c	678	22.4	1.1	40	10	AW231367	AW231367
c	679	22.4	1.1	41	10	BJ058917	BJ058917
	680	22.4	1.1	45	9	AR269955	AR269955
	681	22.4	1.1	46	10	BP085190	BP085190
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c	792	21.8	1.0	52	13	BJ053742	BJ053742
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	802	21.8	1.0	59	9	AR266857	AR266857
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96	20.6	1.0	43	14	T25548	T25548 EST00581 Un
c 96	20.6	1.0	43	17	AU269852	AU269852 AU269852
96	20.6	1.0	44	9	AU269696	AU269696 AU269696
96	20.6	1.0	44	12	BF531819	BF531819 602872738
96	20.6	1.0	44	12	BG969757	BG969757 602787589
96	20.6	1.0	45	9	AU259384	AU259384 AU259384
c 96	20.6	1.0	45	17	AZ624992	AZ624992 IMAGE1A08
97	20.6	1.0	46	9	AU269071	AU269071 AU269071
c 97	20.6	1.0	47	9	AA152855	AA152855 zk4f01.r
c 97	20.6	1.0	47	12	BJ030029	BJ030029 BJ030029
c 97	20.6	1.0	48	13	BJ039490	BJ039490 BJ039490
97	20.6	1.0	49	9	AA657267	AA657267 vr27d07.r
c 97	20.6	1.0	49	14	G20872	G20872 HUMGS000493
c 97	20.6	1.0	49	17	DP15J219	AL716170 Danio rer
c 97	20.6	1.0	50	9	AL798379	AL798379 AL798379
c 97	20.6	1.0	50	13	BJ062166	BJ062166 BJ062166
97	20.6	1.0	50	14	BQ666119	BQ666119 pb16b07.y
98	20.6	1.0	50	14	BQ666711	BQ666711 pb17a07.y
98	20.6	1.0	50	17	AZ347604	AZ347604 IMAGE3C13
98	20.6	1.0	50	17	AZ429164	AZ429164 IMAGE3F05
98	20.4	1.0	22	2	HSM002953	AI038477 Homo sapi
98	20.4	1.0	22	17	BE900233	BE900233 2H02871.21
98	20.4	1.0	22	17	TA3080C5P	AL497363 T. brucei
98	20.4	1.0	23	9	AI418776	AI418776 HF03p76FR
98	20.4	1.0	23	17	AZ215410	AZ215410 IMAGE1C01
98	20.4	1.0	24	9	AI418765	AI418765 HF03p56FM
98	20.4	1.0	25	10	AV737092	AV737092 AV737092
c 99	20.4	1.0	26	17	AZ350816	AZ350816 IMAGE1H21
c 99	20.4	1.0	27	14	T24515	T24515 yr55d01.r1
99	20.4	1.0	28	2	HSM001250	AI037926 Homo sapi
c 99	20.4	1.0	29	2	HSM001546	AI037521 Homo sapi
99	20.4	1.0	29	9	AI018694	AL518694 DKFZp566
99	20.4	1.0	30	2	HSM001965	AI037634 Homo sapi
99	20.4	1.0	30	2	HSM002253	AI037920 Homo sapi
c 99	20.4	1.0	30	2	HSM002906	AI038430 Homo sapi
c 99	20.4	1.0	30	2	HSM003047	AI038571 Homo sapi
c 99	20.4	1.0	30	2	HSM003316	AI038840 Homo sapi
100	20.4	1.0	30	9	AL048729	AL048729 DKFZp5661

ALIGNMENTS

RESULT 1
AA966391
LOCUS AA966391 50 bp mRNA linear EST 31-JUL-1998
DEFINITION [illegible] Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone w4f01al 5', mRNA sequence.
ACCESSION AA966391
VERSION AA966391.1 GI:3140473
KEYWORDS EST.
SOURCE Emericella nidulans.
ORGANISM Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 50)
AUTHORS Kapter,D., Cray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Farrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: T3.
FEATURES Location/Qualifiers
source 1..50
/organism="Emericella nidulans"
/strain="[illegible]"
/db_xref="taxon:162425"
/clone="w4f01al"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK+; Site_1: EcoRI site; Site_2: XhoI, 3' end of cDNA cloned into EcoRI site of pBluescript"
3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 12 a 15 c 13 g 10 t
ORIGIN

Query Match 1.6%; Score 85; DB 9; Length 50;
Best Local Similarity 66.4%; Pred. No. 9.4e-04;
Matches 29; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 1 [illegible] 47
RESULT 2
AL587964/c
LOCUS AL587964 bp mRNA linear EST [illegible]
DEFINITION AL587964 DF Chicken brain library, Gallus gallus cDNA 5', mRNA sequence.
ACCESSION AL587964
VERSION AL587964.1 GI:[illegible]
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 48)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Fraser Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: fraser.murray@bbsrc.ac.uk
[illegible] Poly A RNA purified [illegible] (*6854-
Seq primer: M13F.
FEATURES Location/Qualifiers
source 1..48
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="BP_Sc56f"
/clone_lib="BP Chicken Brain Library"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="[illegible]"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: 5'dGdC, 5' adaptor sequence: 5' [illegible] 3'; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purified [illegible] Clonetech (*6854-1)"
BASE COUNT [illegible] 2 c 2 g [illegible] others
ORIGIN

```
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Pietrik,E.,N., Shapiro,J.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Stephoe,M., Tan,F., Underwood,K., Moore,M.,
            Theisinq,R., Wylie,T., Jennoe,C., Soares,B., Wilcox,L. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:563507.
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:991227"
                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                     /tissue_type="blastocyst"
                     /dev_stage="embryo (pre-implantation)"
                     /lab_host="DH10B"
                     /note="Organ: embryo; Vector: pCMVSPORT; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally from mRNA prepared
                     from 800 blastocysts.  Primer: SalI(dT):
                     5'-CGGTCGACTCTAGAGGATCCTTTTTTTTTTTTTTT-3'; cDNA
                     cloned into the NotI/SalI sites of a pCMVSPORT vector (Life
                     Technologies).  Two different size selections:  B1 (larger
                     inserts) and B2."
BASE COUNT       47 a      1 c      1 g      1 t
ORIGIN

  Query Match             1.6%;  Score 33.8;  DB 9;  Length 50;
  Best Local Similarity   84.4%;  Pred. No. 1.5e-05,
  Matches   38;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 TTTATTTTTTAAAATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47
          |||| | | | |||  ||||||||||||||||||||||||||||||
Db      1 AAGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 45


RESULT 6
HSM809447
ID   HSM809447  standard; DNA; EST; 49 BP.
XX
AC   AL037023;
XX
SV   AL037023.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564H1964_r1  (from clone DKFZp564H1964)
XX
KW   EST, expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-49
RA   Lehrach H., Drescher B., Meier-Ewert S., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MPI for Molecular Genetics, Ihnestr. 73, 14195 Berlin-Dahlem, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by clones within the cDNA
CC   sequencing consortium at the German Human Genome Project.
CC   No additional sequence available.
CC   This clone is available at the RZPD in Berlin
CC   Please contact "HTC-RZPD: Heavy Chain Project" Bereich Lehrach, 14195
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..49
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564H1964"
FT                   /clone_lib="564 (synonym: Hlhr2). Vector pAS; 1.5-4
FT                   kb cDNA, sites NotI - SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 49 BP; 19 A; 8 C; 8 G; 4 T; 10 other;

  Query Match             1.6%;  Score 33.8;  DB 2;  Length 49;
  Best Local Similarity   84.4%;  Pred. No. 1.6e-05;
  Matches   38;  Conservative    0;  Mismatches    4;  Indels    3;  Gaps    3;

Qy      2 TTTATTTTTTAAAATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 47
          |||| | | | |||  ||||||||||||||||||||||||||||||
Db      1 AAGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 45


RESULT 7
AA116935
ID   [illegible]
DEFINITION  mm22g01.r1 Soares mouse embryonic tissue Mus musculus cDNA
            clone IMAGE:991227 5' mRNA sequence.
ACCESSION   AA116935
VERSION     AA116935.1  GI:1671481
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Pietrik,E.,N., Shapiro,J.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Stephoe,M., Tan,F., Underwood,K., Moore,M.,
            Theisinq,R., Wylie,T., Jennoe,C., Soares,B., Wilcox,L. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:425646
            Seq primer: -10m13 EI.
FEATURES             Location/Qualifiers
     source          1..49
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:548704"
                     /clone_lib="Soares mouse embryonic tissue"
                     /sex="pooled"
                     /tissue_type="embryo"
                     /dev_stage="7.5dpc"
                     /lab_host="DH10B"
                     /note="Organ: whole embryo; Vector: pCMV SPORT; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
```

```
VERSION     BF582680.1  GI:11656398
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   NIH-MGC Data Group,Gerhard,D.S.,Wagner,L.,Feingold,E.A.,
            Shenmen,C.M.,Grouse,L.H.,Schuler,G.,Klein,S.L.,Old,S.,Rasooly,R.,
            Good,P.,Guyer,M.,Peck,A.M.,Derge,J.G.,Lipman,D.,Collins,F.S.,
            Jang,W.,Sherry,S.,Feolo,M.,Misquitta,L.,Lee,E.,Rotmistrovsky,K.,
            Greenhut,S.F.,Schaefer,C.F.,Buetow,K.,Bonner,T.I.,Haussler,D.,
            Kent,J.,Kiekhaus,M.,Furey,T.,Brent,M.,Prange,C.,Schreiber,K.,
            Shapro,N.,Bugarski,K.A.,Cai,J.,Cline,E.,Cline,J.,Corbett,M.,
            Dijamco,J.,Edwards,S.,Fakhrai,H.,Gleason,M.,Gunaratne,P.,Han,A.,
            Hu,M.,Kodira,C.,Kovar,C.,Lacy,E.,Lee,E.,Li,W.,Mandrekar,J.,
            Miller,A.,Muzny,D.,Nelson,J.,Parker,N.,Phillips,R.,Purcell,S.,
            Rachupka,A.,Raymond,A.,Robbins-Pianka,A.,Santibanez,J.,Shen,H.,
            Shen,S.,Simmons,B.,Sinogeikin,M.,Strong,G.,Thomas,A.,Tirumalai,R.,
            Tsung,K.,Verduzco,D.,Wan,X.,Wang,Q.,Williams,J.,Yang,J.,Zhou,J.,
            Zimmerman,R.,Rakeman,J.F.,Knipp,M.,Lee,N.,Ayodeji,B.,Allen,L.,
            Ansari,M.,Anyiwo,A.,Attaluri,P.K.,Bedell,J.A.,Bhonagiri,V.,
            Bouffard,G.G.,Burrill,W.D.,Chen,H.C.,Cherukuri,P.F.,Dekhtyar,M.,
            Dickson,M.,Gabisi,R.A.,Garcia,A.M.,Garcia,R.,Gardner,K.,
            Grabrukovich,A.,Han,J.,Hargrove,A.,Hu,P.,Huang,P.,Ingram,R.,
            Legaspi,R.,Maduro,Q.L.,Maduro,V.B.,Masiello,C.A.,Maskeri,B.,
            McDowell,J.,Monaco,C.,Montgomery,K.,Parry,C.,Portnoy,M.,
            Quick,E.,Riggs,M.,Morgan,M.R.,Saranga,D.,Schandler,K.,Stanley,J.R.,
            Sykes,R.,Szpankowski,F.,Tavakoli,A.,Thomas,D.,Thomas,J.,Tsurgeon,C.,
            Villalon,D.,Wang,Y.,Wetherby,K.D.,Wylie,K.,Xing,Y.,Yaylaoglu,M.N.,
            Park,J.,Chinwalla,A.T.,Mardis,E.R.,Wilson,R.K.,Hillier,L.W.,
            Marra,M.A.,Waterston,R.H. and Green,E.D.
  TITLE     The status, quality, and expansion of the NIH full-length cDNA
            project: the Mammalian Gene Collection (MGC)
  JOURNAL   Genome Res. 14 (10B), 2121-2127 (2004)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LIA09772  Row: I  Column: 23
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1..45
                     /organism="Mus musculus"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4236677"
                     /clone_lib="NCI_CGAP_Pr28"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Vector: pCMV-SPORT6; Site_1: Not I;
                     Site_2: Salf; Cloned unidirectionally; Primer: Oligo dT;
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT        44 a        0 c        1 g        0 t
ORIGIN

  Query Match             1.6%;  Score 13.2;  DB 12;  Length 45;
  Best Local Similarity   92.1%;  Pred. No. 1.9e+05;
  Matches   35;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGCCAAAGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCAAAGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 45


RESULT 11
AI793866
LOCUS       AI793866                  42 bp    mRNA    linear   EST 27-JUN-2002
DEFINITION  AI793866 XGP Silurana tropicalis cDNA clone IN4c111114 5',
            mRNA sequence.
ACCESSION   AI793866
VERSION     AI793866.1  GI:21579570
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Taylor,R., Ashurst,J.L., Grafham,M.R., Bird,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2002
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Taylor R
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: IN4c111114.plcSP6
            Sequencing primer: PlcSP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1..42
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="IN4c111114"
                     /clone_lib="NCI_CGAP_Pr28"
                     /dev_stage="neurula"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: Not I;
                     Site_2: Salf; Cloned unidirectionally; Primer: Oligo dT;
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT        40 a        1 c        1 g        0 t
ORIGIN

  Query Match             1.6%;  Score 13.2;  DB 12;  Length 42;
  Best Local Similarity   92.1%;  Pred. No. 1.9e+05;
  Matches   35;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGCCAAAGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCCAAAGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 45


RESULT 12
AI116598
LOCUS       AI116598                  [illegible] bp    mRNA    linear   [illegible]
DEFINITION  [illegible] [illegible] mRNA sequence.
ACCESSION   AI116598
VERSION     AI116598.1  [illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bedell,M., Bielicki,N., Calvert,C.,
            Carter,C., Kucaba,T., Lacy,M., Le,M., Martindale,M., Morris,M.,
            Scherlenberg,K., Stephen,M., Tan,F., Underwood,K., Wagner,L.,
            Yoakum,B., Wylie,T., Louie,T., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     "St. Louis" NIBMG M.musculus EST in pCMV
  JOURNAL   Unpublished (1999)
COMMENT     [illegible]
            Washington University School of Medicine
            Washington University, Genome Sequencing Center
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mgenomes@watson.wustl.edu
            This clone is available royalty free through LLNL [illegible]
            IMAGE Consortium (http://image.llnl.gov) [illegible]
            MGI:[illegible]
            Seq primer: T3 [illegible]
FEATURES             Location/Qualifiers
     source          1..14
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="Schiller mouse MA"16"
                     /cell_line="colon cancer cell line"
                     /lab_host="SCLR"
                     /note="Vector: pBluescript SK- (Stratagene); [illegible]
                     [illegible] XL-1 Blue [illegible] mRNA was isolated from
                     cell line MA" [illegible]
                     [illegible]
                     [illegible] was used to [illegible] the cDNA [illegible]
                     [illegible] was constructed by [illegible]
                     went through [illegible] purification. Average insert
                     size is 1.7 kb, with a range from 0.8 kb [illegible]
                     was constructed by Dr. Martin Schiller ([illegible]
                     University)  "
BASE COUNT        40 a        4 c        1 g        1 t
ORIGIN
```

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            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1..49
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0594020"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, Tl resistant, F-"
                     /note="Vector: pWD42mv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http: [illegible]). DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA [illegible]
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4721211|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid F1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       0 a      2 c      0 g     47 t
ORIGIN

  Query Match             1.6%;  Score 33.2;  DB 17;  Length 49;
  Best Local Similarity   92.1%;  Pred. No. 1.9e+05;
  Matches   35;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2096 AGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
              |||:|  ||||||||||||||||||||||||||||
Db         [illegible] AGA[illegible]AAAAAAAAAAAAAAAAAAAAAA 2


RESULT 16
AA853120/c
LOCUS       AA853120                  50 bp    mRNA    linear   EST 20-JUN-2002
DEFINITION  NHTBCae03e06r1 Normal Human Trabecular Bone Cells Homo sapiens cDNA
            clone NHTBCae03e06, mRNA sequence.
ACCESSION   AA853120
VERSION     AA853120.1  GI:2939859
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
            Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Vaughn,M., Robey
            ,P.G., Hotchkiss,R.N. and Francomano,C.A.
  TITLE     SGAP: The Skeletal Genome Anatomy Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Libin Jia
            Medical Genetics Branch
            National Human Genome Research Institute
            10/10C101 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
            Tel: 301-402-4877
            Fax: 301-496-7157
            Email: libin@helix.nih.gov
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="NHTBCae03e06"
                     /clone_lib="Normal Human Trabecular Bone Cells"
                     /sex="Female"
                     /tissue_type="Bone"
                     /cell_type="Trabecular Bone Cells"
                     /lab_host="SOLR"
                     /note="[illegible]
                     Library constructed by Dr. Marian Y[illegible]
                     [illegible] (NIDR)"
BASE COUNT    [illegible]
ORIGIN

  Query Match             1.6%;  Score 33.2;  DB 9;  Length 50;
  Best Local Similarity   92.1%;  Pred. No. 1.9e+05;
  Matches   35;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2096 AGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
              |||:|  ||||||||||||||||||||||||||||
Db         17 [illegible]AAAAAAAAAAAAAAAAAAAAAAAA 54


RESULT 17
AA607953
LOCUS       AA607953                  [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  vm39h06.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA
            clone IMAGE:992[illegible] 5', mRNA sequence.
ACCESSION   AA607953
VERSION     AA607953.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 5[illegible])
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:564883.
FEATURES             Location/Qualifiers
     source          1..5[illegible]
                     /organism="Mus musculus"
                     /strain="C57BL/6 x DBA/2 F1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:992[illegible]"
                     /clone_lib="Knowles Solter mouse blastocyst B1"
                     /tissue_type="blastocyst"
                     /dev_stage="embryo (pre-implantation)"
                     /lab_host="DH10B"
                     /note="Organ: embryo; Vector: pSPORT1; Site_1: NotI;
                     Site_2: SalI; [illegible]
                     from [illegible] blastocysts. [illegible] SalI(dT)
                     [illegible]
                     [illegible] the NotI/SalI sites of a pSPORT1 [illegible]
                     [illegible]. Two different size selections [illegible]
                     inserts) and B1."
BASE COUNT    45 a    [illegible]
ORIGIN

  Query Match             1.6%;  Score 33.2;  DB 9;  Length 5[illegible];
  Best Local Similarity   82.6%;  Pred. No. 1.9e+05;
```

```
            Fax. 314 286 1810
            Email: monsoest@watson.wustl.edu
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:481216.
FEATURES             Location/Qualifiers
     source          1..49
                     /organism "Mus musculus"
                     /strain "C57BL/6J x DBA/2J F1"
                     /db_xref "taxon:10090"
                     /clone="IMAGE:804872"
                     /clone_lib "Knowles Solter mouse blastocyst B1"
                     /tissue_type="blastocyst"
                     /dev_stage="embryo (pre-implantation)"
                     /lab_host="DH10B"
                     /note="organ: embryo; Vector: pSPORT; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally from mRNA prepared
                     from 800 blastocysts.  Primer: SalI(dT):
                     5'-GCGTCGACCCTTCACCCTTTTTTTTTTTTTT-3'.  cDNA was
                     cloned into the NotI/SalI sites of a pSPORT vector (Life
                     Technologies).  Two different size selections: M1 (larger
                     inserts) and B3."
BASE COUNT       42 a       1 c       5 g       1 t
ORIGIN

  Query Match           1.5%;  Score 33;  DB 9;  Length 49;
  Best Local Similarity   79.6%;  Pred. No. 2e+05;
  Matches   39;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2084 AAGTAATGACTTAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2137
           ||| || ||   |  ||  ||||||||||||||||||||||||||||||||||
Db       1 AAGAAAAGAGAGAAGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 49


RESULT 21
BI496942
LOCUS       BI496942                  50 bp    mRNA    linear   EST 28 AUG 2001
DEFINITION  hl29g19.y1 Morton Fetal Cochlea Homo sapiens cDNA clone
            IMAGE:2537658 5', mRNA sequence.
ACCESSION   BI496942
VERSION     BI496942.1  GI:15836286
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bielat,F.H.
            and Morton,C.C.
  TITLE     Isolation of novel and known genes from a human fetal cochlear cDNA
            library using subtractive hybridization and differential screening
  JOURNAL   Genomics 23, 12-50 (1994)
  MEDLINE   95139111
COMMENT     Contact: Morton, C. C.
            Departments of Pathology and Obstetrics, Gynecology and
            Reproductive Biology
            Brigham and Women's Hospital
            75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
            Tel: 617 732 7980
            Fax. 617 738 6996
            Email: cmorton@bics.bwh.harvard.edu
            DNA sequencing and analyses were performed by National Institutes
            of Health Intramural Sequencing Center (NISC, see
            http://www.nisc.nih.gov).
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Plate: LLAM6320  row: M  column: 19
            Seq primer: M13REV reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone="IMAGE:2537658"
                     /clone_lib "Morton Fetal Cochlea"
                     /tissue_type "cochlea"
                     /dev_stage "16-22 week fetus"
                     /lab_host "DH5 cells (kanamycin resistant)"
                     /note "Organ: ear; Vector: pBluescript SK-; Site_1: EcoRI;
                     Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
                     unidirectionally. Primer: Oligo dT. Fetal cochlear tissue
                     17% of inserts >1.5 kb, 77% >0.5 kb, 7% <0.5 kb. Not
                     normalized or subtracted. Sequenced at the Washington
                     University Genome Sequencing Center. 5' adaptor sequence:
                     5' GAATTCGGCACGAGGGTCGACGGTATCGATAAGCTT 3'.  3' adaptor
                     sequence: 5' CTCTAGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT       47 a       1 c       2 g       0 t
ORIGIN

  Query Match           1.5%;  Score 33;  DB 9;  Length 50;
  Best Local Similarity   79.6%;  Pred. No. 2e+05;
  Matches   39;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy    2085 AGTAATGACTTAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2134
           || ||  |  | ||  ||||||||||||||||||||||||||||||||||
Db       2 AGAAAAGAGAGAAGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50


RESULT 22
AL628936/c
LOCUS       AL628936                  48 bp    mRNA    linear   EST 28 AUG 2001
DEFINITION  AL628936.1 Xenopus tropicalis gill tadpole cDNA clone TGPA-C-1p1 5',
            mRNA sequence.
ACCESSION   AL628936
VERSION     AL628936.1  GI:16598419
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   [illegible], Taylor J., Ashurst J., Dunn A.M. and Loosli F.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (JGI_2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Buckle E
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: tropi@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: Gasellpl5.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1..48
                     /organism="Silurana tropicalis"
                     /db_xref "taxon:8364"
                     /clone "TGasellpl5"
                     /clone_lib "XGC-unstrula"
                     /dev_stage="gastrula (stages 10.5-13 groups)"
                     /lab_host "Escherichia coli XL1-Blue"
                     /note "Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA isolated
                     [illegible]. Double NotI and cDNA was then ligated
                     into pCS107 with EcoRI at the 5' end and NotI at the 3'
                     end."
BASE COUNT       14 a       9 c       9 g      16 t
ORIGIN

  Query Match           1.5%;  Score 33;  DB 9;  Length 48;
  Best Local Similarity   89.7%;  Pred. No. 2e+05;
  Matches   35;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    2085 AGTAATGACTTAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2134
           || ||  |||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGAAAAGAGAGAAGAATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 48
```

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                    a Not I - oligo(dT) primer. Double stranded cDNA was
                    ligated to Eco RI adaptors (Pharmacia), digested with Not
                    I and cloned into the Not I and Eco RI sites of the
                    modified pT7T3 vector.  Library is not normalized. Library
                    was constructed by Benito Soares and M. Fatima Bonaldo. "
BASE COUNT        3 a       3 c       2 g      42 t
ORIGIN

  Query Match              1.5%;  Score 2.6;  DB 9;  Length 50;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-05;
  Matches   45;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3095 TAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3143
             | ||||  ||||||||||||||||||||||||||||||||||
Db        44 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6


RESULT 26
AW433255
LOCUS       AW433255                  50 bp    mRNA    linear   EST 11-JAN-2000
DEFINITION  CM0-AG0-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
            sequence.
ACCESSION   AW433255
VERSION     AW433255.1  GI:6823612
KEYWORDS    EST.
SOURCE      Pneumocystis carinii f. sp. carinii.
  ORGANISM  Pneumocystis carinii f. sp. carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Idman
            ,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Pneumocystis carinii f. sp. carinii"
                     /db_xref="taxon:[illegible]"
                     /clone_lib="AGS-1"
                     /clone="CM0-AG0-1"
                     /note "Vector: Lambda ZAP II; Site 1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (8x10e8) from a steroid rat (99.1%
                     sacrificed on 5/17/99) at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT primed, standard
                     conditions described by Soares, Stratagene. Further
                     details see www.sky.edu/~ [illegible]."
BASE COUNT        9 a       1 c       2 g      38 t
ORIGIN

  Query Match              1.5%;  Score 2.6;  DB 10;  Length 50;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-05;
  Matches   45;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2994 TTAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3042
             ||| |||  ||||||||||||||||||||||||||||||||||
Db        50 TTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 27
BQ258029
LOCUS       BQ258029                  50 bp    mRNA    linear   EST 07-MAY-2002
DEFINITION  NIH_BMAP_MGC_250 Homo sapiens cDNA clone IMAGE:5408895, mRNA
            sequence.
ACCESSION   BQ258029
VERSION     BQ258029.1  GI:20458782
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
REFERENCE   1  (bases 1 to 50)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project,
            Tumor Gene Index
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: I. Baker (Stanford University)
             cDNA Library Arrayed by: the I.M.A.G.E. Consortium/L.N.
             LNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution, additional
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
             MGC:[illegible],
            Plate: [illegible] Row: [illegible] Col: [illegible]
            Seq primer: Sp6 primer.
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Homo sapiens"
                     /strain="[illegible]"
                     /db_xref="taxon:[illegible]"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="Soares [illegible]"
                     /tissue_type="embryo, late gestation"
                     /dev_stage="embryo, 7.5 dpc"
                     /lab_host="XL1 Blue"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: NotI; cDNA
                     made by oligo dT priming, directionally cloned at
                     SalI/NotI sites using the following 5' adapt:
                     5'-[illegible]', size-selected for >1.0 kb; Library
                     size: 1.0-3.0 kb; Library constructed by I. Baker (Stanford
                     University)."
BASE COUNT       40 a       5 c       3 g       2 t
ORIGIN

  Query Match              1.5%;  Score 2.6;  DB 10;  Length 50;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-05;
  Matches   45;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2994 TTAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3042
             ||| |||  ||||||||||||||||||||||||||||||||||
Db        50 TTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 28
BQ258029
ID   BQ258029 standard; DNA; EST; 50 BP.
XX
AC   AL038433;
XX
SV   AL038433.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST; [illegible] (from clone [illegible])
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Eutheria; Euarchontoglires; Primates; Haplorrhini;
XX
RN   [1]
RP   1-42
RA   [illegible]
RC   [illegible]
```

```
RC   Data were filed (12 MAR 2003) to the EMBL/GenBank/DDBJ databases.
RA   Mayer A., Kloppenburg P., Strauss H.P., Martinsried, GERMANY
XX
RT   "Identification of Wisconsin sequenced Mod Genomics within the cDNA
RT   collection contributed to the German Genome Project"
RT   ; sequence also available
RT   ; file is also available at the EBI in Berlin
RT   ; submitted the Klein Wassergrundcentrum, Beuhnerweg 6, 10557
RT   Berlin-Charlottenburg, GERMANY; Email: clone@rpfinder
XX
RL   Reference Location/Qualifiers
RN
RP   1-1234
RC   /db_xref "taxon:9606"
RC   /cell_line="HeLa sequences"
RC   /clone="EKEJp666A0424"
RC   /clone_lib "Eco (synonyme: bikd.), Vector pAMES: Host
RC   XL-Blue; sites NotI + SalI"
RC   /dev_stage "Fetal"
RC   /tissue_type "kidney"
XX
RG   Genome Project Consortium
XX
RA   Mayer A., Kloppenburg P., Strauss H.P., Martinsried, GERMANY
XX
RT   "Identification of Wisconsin sequenced Mod Genomics within the cDNA
RT   collection contributed to the German Genome Project"
RT   ; sequence also available
RT   ; file is also available at the EBI in Berlin
RT   ; submitted the Klein Wassergrundcentrum, Beuhnerweg 6, 10557
RT   Berlin-Charlottenburg, GERMANY; Email: clone@rpfinder
XX
RL   Reference Location/Qualifiers
RN
RP   1-1234
RC   /db_xref "taxon:9606"
RC   /cell_line="HeLa sequences"
RC   /clone="EKEJp666A0424"
RC   /clone_lib "Eco (synonyme: bikd.), Vector pAMES: Host
RC   XL-Blue; sites NotI + SalI"
RC   /dev_stage "fetal"
RC   /tissue_type "kidney"
XX
RG   Genome Project Consortium
XX
RA   Mayer A., Kloppenburg P., Strauss H.P., Martinsried, GERMANY
XX
RT   "Identification of Wisconsin sequenced Mod Genomics within the cDNA
RT   collection contributed to the German Genome Project"
RT   ; sequence also available
RT   ; file is also available at the EBI in Berlin
RT   ; submitted the Klein Wassergrundcentrum, Beuhnerweg 6, 10557
RT   Berlin-Charlottenburg, GERMANY; Email: clone@rpfinder
XX
RL   Reference Location/Qualifiers
RN
RP   1-1234
RC   /db_xref "taxon:9606"
RC   /cell_line="HeLa sequences"
RC   /clone="EKEJp666A0424"
RC   /clone_lib "Eco (synonyme: bikd.), Vector pAMES: Host
RC   XL-Blue; sites NotI + SalI"
RC   /dev_stage "fetal"
RC   /tissue_type "kidney"
XX
RG   Genome Project Consortium
XX
RA   Mayer A., Kloppenburg P., Strauss H.P., Martinsried, GERMANY
XX
RT   "Identification of Wisconsin sequenced Mod Genomics within the cDNA
RT   collection contributed to the German Genome Project"
RT   ; sequence also available
RT   ; file is also available at the EBI in Berlin
RT   ; submitted the Klein Wassergrundcentrum, Beuhnerweg 6, 10557
RT   Berlin-Charlottenburg, GERMANY; Email: clone@rpfinder
XX
RL   Reference Location/Qualifiers
RN
RP   1-1234
RC   /db_xref "taxon:9606"
RC   /cell_line="HeLa sequences"
RC   /clone="EKEJp666A0424"
RC   /clone_lib "Eco (synonyme: bikd.), Vector pAMES: Host
RC   XL-Blue; sites NotI + SalI"
```

```
AA574989
LOCUS       AA574989                  50 bp    mRNA    linear   EST 02-SEP-1997
DEFINITION  [illegible] Knowles Solter mouse blastocyst [illegible] EST,
            clone IMAGE:992044 5', mRNA sequence.
ACCESSION   AA574989
VERSION     AA574989.1  GI:2449615
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Stephen,M., Pan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
  COMMENT   Contact: Marra M/M...
            WashU HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available [illegible] IMAGE Consortium
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:564324.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Mus musculus"
                     /strain="[illegible] F1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:992044"
                     /clone_lib="Knowles Solter mouse blastocyst B1"
                     /tissue_type="[illegible]"
                     /dev_stage="embryo (pre-implantation)"
                     /lab_host="DH10B"
                     /note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally from mRNA prepared
                     from 800 blastocysts.  Primer: SalI(dT):
                     5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. cDNAs were
                     cloned into the NotI/SalI sites of a pSPORT vector (Life
                     Technologies).  Two different size selections: B1 (larger
                     inserts) and B3."
BASE COUNT       44 a      0 c      6 g      0 t
ORIGIN

  Query Match              1.5%;  Score 32.4;  DB 6;  Length 50;
  Best Local Similarity   78.0%;  Pred. No. 2.5e-05;
  Matches   39;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      2084 AAGTAATGACTTAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
             ||  || ||   | | |  |||| ||||||||||||||||||||||||||
Db         1 AAATAAACAAACGAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50


RESULT 42
BQ524-25/c
LOCUS       BQ524325                  50 bp    mRNA    linear   EST 10-JUN-2002
DEFINITION  NIGC_xs04b03.y1 NIGMS_XGC_Xtr2 Silurana tropicalis cDNA clone
            IMAGE:5279797 5', mRNA sequence.
ACCESSION   BQ524325
VERSION     BQ524325.1  GI:21393194
KEYWORDS    EST
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea, Pipidae,
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   NIH-XGC http://[illegible]
  TITLE     National Institute of Child Health and Human Development (NICHD)
            Cancer Institute, Xenopus Gene Collection
  JOURNAL   Unpublished (2002)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
            cDNA Library Arrayed by: the I.M.A.G.E. Consortium/LLNL
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
            Clone distribution: 5' and 3' clone distribution for this clone is
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM1967  Row: D  Column: 6
            50q primer, M13(-21) reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:5279797"
                     /clone_lib="Nasco Xtr_LAM8"
                     /tissue_type="tadpole"
                     /dev_stage="embryo, stages 40-45"
                     /lab_host="DH10B electroporated"
                     /note="Vector: pCMV SPORT6.0NotI; Site_1: NotI; Site_2:
                     EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average
                     insert size 2.1 kb. Constructed by Invitrogen, Nasco Xtr
                     Xenopus Gene Collection (XGC) library."
BASE COUNT       0 a      0 c      0 g      5 t
ORIGIN

  Query Match              1.5%;  Score 32.4;  DB 14;  Length 50;
  Best Local Similarity   78.0%;  Pred. No. 2.5e-05;
  Matches   39;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      2084 AAGTAATGACTTAGAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
             ||  || ||   | | |  |||| ||||||||||||||||||||||||||
Db         1 AAATAAACAAACGAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 50


RESULT 43
HSM001841
ID   HSM001841  standard; RNA; EST; 40 BP.
XX
AC   AL037510;
XX
SV   AL037510.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST IMAGE:[illegible]  (from clone IMAGE:[illegible]).
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-40
RA   Blum H., Bamberg-Lemper K., Meyer W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz, [illegible] Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by LMU within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No 5' sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD, Ressourcenzentrum, Heubnerweg [illegible]
CC   Berlin Charlottenburg, GERMANY, Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
```

```
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   [illegible]
  TITLE     Sanger Xenopus tropicalis EST project 2001 (10_2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Buckle B
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TNeu026e18.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="TNeu026e18"
                     /clone_lib="XGC [illegible]"
                     /dev_stage="neurula"
                     /lab_host="[illegible]"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from neurula.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT       36 a      5 c      9 g      0 t
ORIGIN

  Query Match             1.5%;  Score 32.2;  DB 9;  Length 50;
  Best Local Similarity   91.9%;  Pred. No. 2.7e-05;
  Matches   [illegible];  Conservative    0;  Mismatches    [illegible];  Indels    0;  Gaps    0;

Qy       2097 GAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133
              ||||   |||||||||||||||||||||||||||||
Db          9 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 45


RESULT 37
AA617223
LOCUS       AA617223                  50 bp    mRNA    linear   EST 07-OCT-1997
DEFINITION  vj79e05.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA
            clone IMAGE:935264 5', mRNA sequence.
ACCESSION   AA617223
VERSION     AA617223.1  GI:2504428
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:549184.
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:935264"
                     /clone_lib="Knowles Solter mouse blastocyst B1"
                     /tissue_type="blastocyst"
                     /dev_stage="embryo (pre-implantation)"
                     /lab_host="DH10B"
                     /note="Organ: embryo; Vector: pSPORT1; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally from cDNA prepared
                     from 800 blastocysts.  Primer: SalI(dT);
                     [illegible]
                     cloned into the NotI/SalI sites of a pSPORT1 vector (Life
                     Technologies).  Two different size selections [illegible]
                     inserts) and [illegible]."
BASE COUNT       40 a      6 c      3 g      1 t
ORIGIN

  Query Match             1.5%;  Score 32.2;  DB 9;  Length 50;
  Best Local Similarity   91.9%;  Pred. No. 2.7e-05;
  Matches   [illegible];  Conservative    0;  Mismatches    [illegible];  Indels    0;  Gaps    0;

Qy       2097 [illegible] 2133
              ||||   |||||||||||||||||||||||||||||
Db         11 [illegible] 47


RESULT 38
AW215755
LOCUS       AW215755                  50 bp    mRNA    linear   EST [illegible]
DEFINITION  up09f10.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:[illegible]
            mRNA sequence.
ACCESSION   AW215755
VERSION     AW215755.1  GI:6526450
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   NCI-CGAP [illegible] ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            [illegible]/image.html

            MGI:1932015
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Mus musculus"
                     /strain="ZEH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="NCI_CGAP_Lu30"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Transgenic model WNT-1 expression [illegible]
                     MMTV-LTR enhancer; Cloned unidirectionally [illegible]
                     dT.  Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT       [illegible] a      2 c      8 g      1 t
ORIGIN

  Query Match             1.5%;  Score 32.2;  DB 10;  Length 50;
  Best Local Similarity   [illegible];  Pred. No. 2.7e-05;
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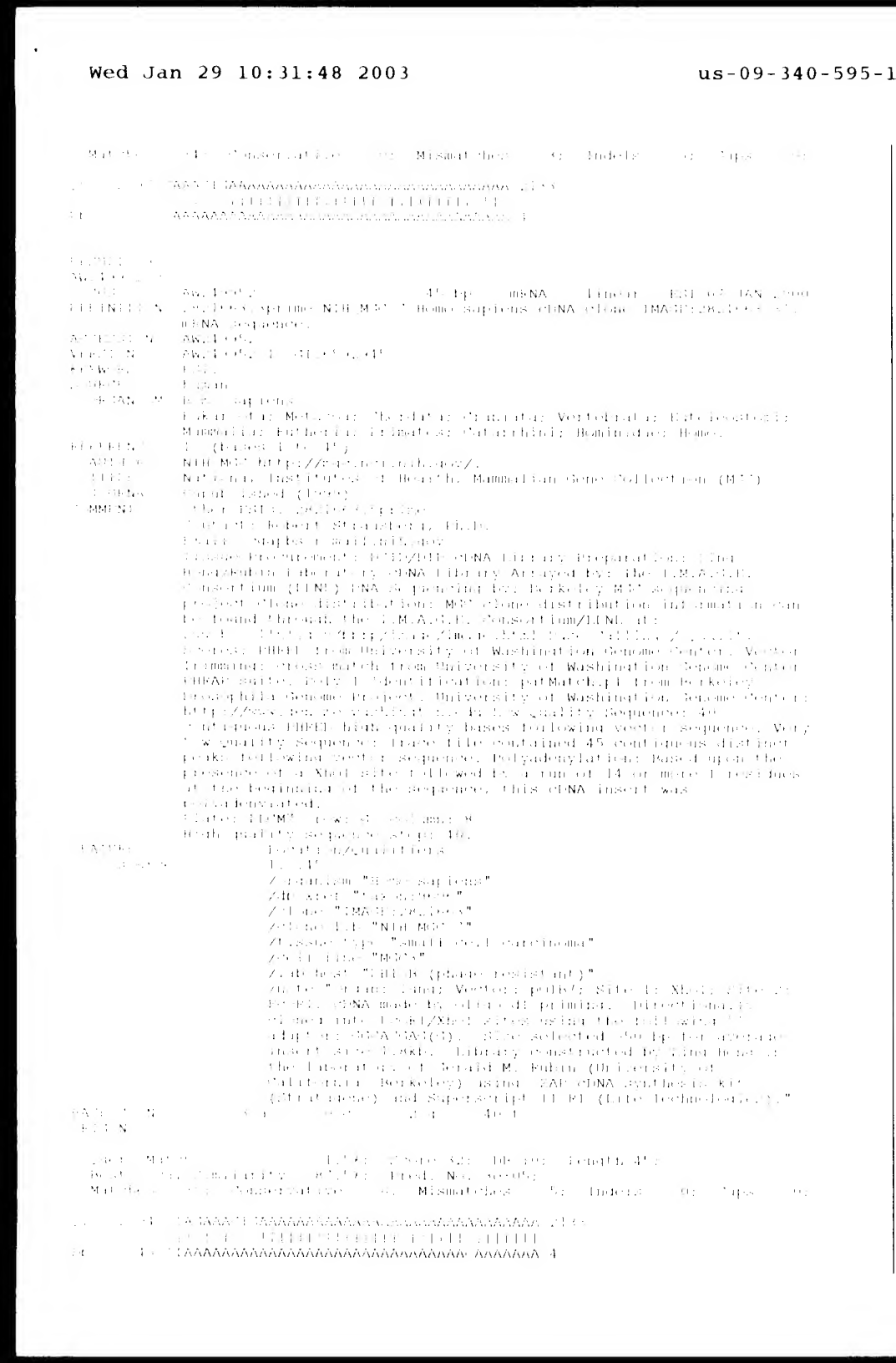

```
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-49
RA   Bloecker H., Beyreuther K., Brandt P., Mertes W., Carstenbaer J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 19a, D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No sl sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..49
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="IRFPp564C124"
FT                   /clone_lib="566 (synonym: hbm3) Vector pAMP1; host
FT                   XL-2Blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="kidney"
XX
SQ   Sequence 49 BP; 27 A; 6 C; 10 G; 2 T; 0 other;

  Query Match              1.5%;  Score 42;  DB 2;  Length 49;
  Best Local Similarity   87.5%;  Pred. No. 2.9e-05;
  Matches   35;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      2094 TTACAAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2138
             ||| |||   |||||||| |||||||||||||||||||||
Db        10 TTAAAAAAAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAA 49


RESULT 42
AA589132
LOCUS       AA589132                 49 bp    mRNA    linear   EST 15-FEB-1999
DEFINITION  vi54g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:907552 5', mRNA sequence.
ACCESSION   AA589132
VERSION     AA589132.1  GI:2405033
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euprimates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Bielicki,N.,
            Gelfand,Y., Kucaba,T., Iadanoto,S., Lennon,G., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,L., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:528216
            Seq primer: -28m13 rev1 DT from Amersham.
FEATURES             Location/Qualifiers
     source          1..49
                     /organism="Mus musculus"
                     /strain="C57BL/6 x DBA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:907552"
                     /clone_lib="Soares fetal liver spleen 1NFLS S1"
                     /sex="pooled"
                     /tissue_type="embryo"
                     /dev_stage="7.5dpc"
                     /lab_host="DH12S"
                     /note="Vector: pCMV-SPORT; Site_1: Not1; Site_2: Sal1;
                     Oligo dT. Gastrulating embryos were collected at 7.5 dpc
                     from C57BL/6 x DBA matings. Excluding embryos that had
                     developed head folds and all extraembryonic tissues.
                     Average insert size: 1.4 Kb (range: 0.8 - 3.0 Kb).
                     Referenced in Development 121, 2479-2490 (1995)"
BASE COUNT        16 a        6 c       10 g        2 t        0 others
ORIGIN

  Query Match              1.5%;  Score 42;  DB 2;  Length 49;
  Best Local Similarity   87.5%;  Pred. No. 2.9e-05;
  Matches   35;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      2094 TTACAAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2138
             ||| |||   |||||||| |||||||||||||||||||||
Db        10 TTAAAAAAAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAA 49


RESULT 43
HSM002879/c
ID   HSM002879  standard; DNA; EST; 50 BP.
XX
AC   AL037748;
XX
SV   AL037748.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA; EST DKFZp564C227_s1  (from clone DKFZp564C227).
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-50
RA   Bloecker H., Beyreuther K., Brandt P., Mertes W., Carstenbaer J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL   MIPS, Am Klopferspitz 19a, D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by GBF within the cDNA
CC   sequencing consortium of the German Genome Project
CC   No sl sequence available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..50
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DKFZp564C227"
FT                   /clone_lib="564 (synonym: hbm2). Vector pAMP1; host
FT                   XL-2Blue; sites NotI + SalI"
FT                   /dev_stage="fetal"
FT                   /tissue_type="brain"
XX
SQ   Sequence 50 BP; 7 A; 9 C; 18 G; 6 T; 0 other;

  Query Match              1.5%;  Score 42;  DB 2;  Length 50;
```

```
            High quality sequence stop: 44.
FEATURES             Location/Qualifiers
     source          1..44
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3992864"
                     /clone_lib="NIH_MGC_66"
                     /tissue_type="brain cell line, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primers: oligo dT.
                     Average insert size 1.1 kb.  Library constructed by Life
                     Technologies."
BASE COUNT        32 a        8 c        5 g        6 t
ORIGIN

  Query Match             1.5%;  Score 31.8;  DB 12;  Length 44;
  Best Local Similarity   83.7%;  Pred. No. 3.4e+05;
  Matches   36;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2099 ATGACTTACAAACTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2131
             ||||||| |  | ||||||||||||||||||||||||||||
Db         2 ATGACTTTTCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44


RESULT 17
AL793626/c
ID   AL793626    standard; mRNA; EST; 38 BP.
XX
AC   AL793626;
XX
DT   01-JUL-2001 (Rel. 66, Created)
DT   01-JUL-2001 (Rel. 66, Last updated, Version 1)
XX
DE   Mouse whole genome scaffolding with paired end reads from a cDNA
DE   plasmid inserts
XX
KW   GSS.
XX
OS   house mouse
OC   Mus musculus
XX
RN   [1]
RP   1-38
RA   Bancroft A., Agarwal A., Barton M., Bentley D., Burton J., Burrill W.,
RA   Islam M., Langford C., Maddy A.M., Meredith D., Porter K., Rice C.,
RA   Rose M., Rose K., Stokes E., Tinsley A., Wall N., Wickremesinghe A.
RA   and Wright D.;
RT   "Mouse whole genome scaffolding with paired end reads from a cDNA
RT   plasmid inserts";
RL   Unpublished (2001).
XX
CC   Contact: Robert D. Weiss
CC   University of Utah, Salt Lake City
CC   Department of Pathology
CC   801 Wakara Way, Salt Lake City, UT 84108, USA
CC   Tel: 801 585 3411
CC   Fax: 801 585 3533
CC   Email: ddna@genetics.utah.edu
CC   Insert length: 1000.0  SD: Error: 0.00
CC   Plate: 3123  row: I  column: 7
CC   Seq primer: AAAAAAAAAATTAA
CC   Class: pUC18/19
CC   High quality sequence start: 1
FH   Key             Location/Qualifiers
FT   source          1..38
FT                   /organism="Mus musculus"
FT                   /strain="C57Bl/6J"
FT                   /db_xref="taxon:10090"
FT                   /clone="3850_2M0028100"
FT                   /clone_lib="Mouse host plasmid UE3CM library"
FT                   /sex="Male"
FT                   /lab_host="E. coli str. XL1-Blue, ampicillin resistant"
FT                   /note="Vector: pWE15; purified genomic DNA was a gift
FT                   from Dr. M.
FT                   Simonius (C57Bl/6J (male) was obtained from the Jackson
FT                   Laboratory Mouse DNA Resource
FT                   [http://www.jax.org/resources/documents/cytogenetics/].
FT                   DNA
FT                   was hydrodynamically sheared by repeated passage through a
FT                   0.005 inch orifice at constant velocity. The sheared DNA
FT                   was blunt end repaired with T4 DNA polymerase and T4
FT                   polynucleotide kinase. Adaptor oligonucleotides were
FT                   ligated to the blunt ends in high molar excess. The
FT                   adaptored DNA was purified and size separated [1.5 kb].
FT                   1.5 kb bands using preparative agarose
FT                   electrophoresis. Vector DNA was prepared from pWE15
FT                   (pWE15cI1consAscI 7.2) by digestion
FT                   independent preparations of plasmid DNA. The DNA was ligated
FT                   with adapters complementary to the insert adaptors and
FT                   purified. The sheared, adaptored mouse DNA was ligated to
FT                   adaptored vector DNA, and transformed into
FT                   chemically competent E. coli XL1-Blue MRF' (Stratagene) by
FT                   and selected for ampicillin resistance"
BASE COUNT
ORIGIN

  Query Match             1.5%;  Score 31.8;  DB 12;  Length 38;
  Best Local Similarity   89.5%;  Pred. No. 3.4e+05;
  Matches   34;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2099 ATGACTTACAAACTCGAAAAAAAAAAAAAAAAAAAAAA 2134
             |||| |||||||||||||||||||||||||||||||||
Db         1 ATGATTTTCTGAAAAAAAAAAAAAAAAAAAAAAAAAA 38
```